

SEQUENCE LISTING

<110> ASAHI KASEI KABUSHIKI KAISHA

<120> NF- κ B Activating Gene

<130> F101131-US

<150> JP 2000-402288

<151> 2000-12-28

<150> JP 2001-088912

<151> 2001-03-26

<150> JP 2001-254018

<151> 2001-08-24

<150> US 60/258,315

<151> 2000-12-28

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<151> 2001-08-24

<160> 224

<170> PatentIn Ver. 2.0

<210> 1

<211> 167

<212> PRT

<213> Homo sapiens

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Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr
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Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser
35 40 45

Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln
50 55 60

Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly
65 70 75 80

Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly
85 90 95

Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr
100 105 110

Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro

115

120

125

Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser

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Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly

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Tyr Gly Gly Thr Arg Arg Arg

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<210> 2

<211> 1472

<212> DNA

<213> Homo sapiens

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<222> (194)..(694)

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ggattcctgt aac atg agt gga ttg att acc atc gtg gta ctc ctt ggg 229

Met Ser Gly Leu Ile Thr Ile Val Val Leu Leu Gly

1

5

10

atc gcc ttt gta gtc tat aag ctg ttc ctg agt gac ggg cag tat tct 277

Ile Ala Phe Val Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Tyr Ser

15

20

25

cct cca ccg tac tct gag tat cct cca ttt tcc cac cgt tac cag aga 325

Pro Pro Pro Tyr Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg

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35

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ttc acc aac tca gca gga cct cct ccc cca ggc ttt aag tct gag ttc 373

Phe Thr Asn Ser Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe

45

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60

aca gga cca cag aat act ggc cat ggt gca act tct ggt ttt ggc agt 421

Thr Gly Pro Gln Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser

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70

75

gct ttt aca gga caa caa gga tat gaa aat tca gga cca ggg ttc tgg 469

Ala Phe Thr Gly Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp

80

85

90

aca ggc ttg gga act ggt gga ata cta gga tat ttg ttt ggc agc aat 517

Thr Gly Leu Gly Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn

95

100

105

aga gcg gca aca ccc ttc tca gac tcg tgg tac tac ccg tcc tat cct 565

Arg Ala Ala Thr Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro

110	115	120	
ccc tcc tac cct ggc acg tgg aat agg gct tac tca ccc ctt cat gga	613		
Pro Ser Tyr Pro Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly			
125	130	135	140
ggc tcg ggc agc tat tcg gta tgt tca aac tca gac acg aaa acc aga	661		
Gly Ser Gly Ser Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg			
145	150	155	
act gca tca gga tat ggt ggt acc agg aga cga taaagtagaa agttggagtc	714		
Thr Ala Ser Gly Tyr Gly Gly Thr Arg Arg Arg			
160	165		
aaacactgga tgcagaaatt ttggattttt catcactttc tctttagaaa aaaagtacta	774		
cctgttaaca attgggaaaa ggggatattc aaaagttcgg tgggtgttatg tccagtgtag	834		
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gttattacct catagagact gtaatattht atttggattht atattattht atgtttgctg	1134		
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<211> 339

<212> PRT

<213> Homo sapiens

<400> 3

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20 25 30

Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His

35 40 45

Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu

50 55 60

Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val
65 70 75 80

Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu
85 90 95

Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val
100 105 110

Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly
115 120 125

Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln
130 135 140

Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp
145 150 155 160

Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu
165 170 175

Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu
180 185 190

Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro
195 200 205

Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro

210	215	220
Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His		
225	230	235 240
Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr		
245	250	255
Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile		
260	265	270
Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp		
275	280	285
Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn		
290	295	300
Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys		
305	310	315 320
Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr		
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Arg Arg Arg		

<210> 4

<211> 1924

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (115)..(1131)

<400> 4

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Met

1

gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc 165
Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly

5

10

15

ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac 213
Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp

20

25

30

cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat 261
Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr

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40

45

gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa 309
Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys

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55

60

65

tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata 357
 Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile

70 75 80

cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt 405
 Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys

85 90 95

aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc 453
 Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser

100 105 110

tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct 501
 Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser

115 120 125

tgt ggc ttg gag tat aat tta gat tat aca gaa ctt ggc ctg cag aaa 549
 Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys

130 135 140 145

ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat tat 597
 Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr

150 155 160

tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att 645
 Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile

165 170 175

acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc 693
 Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe
 180 185 190

ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca 741
 Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro
 195 200 205

ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct ccc 789
 Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro
 210 215 220 225

cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggc cat ggt 837
 Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly
 230 235 240

gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa 885
 Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu
 245 250 255

aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta 933
 Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu
 260 265 270

gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg 981
 Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser
 275 280 285

tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg 1029

Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg
 290 295 300 305

gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca 1077
 Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser
 310 315 320

aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg 1125
 Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg
 325 330 335

aga cga taaagtagaa agttggagtc aaacactgga tgcagaaatt ttggattttt 1181
 Arg Arg

catcactttc tctttagaaa aaaagtacta cctgttaaca attgggaaaa ggggatattc 1241

aaaagttcgg tgggtgttatg tccagtgtag ctttttgtat tctattattt gaggctaaaa 1301

gttgatgtgt gacaaaatac ttatgtgttg tatgtcagtg taacatgcag atgtatattg 1361

cagtttttga aagtgatcat tactgtggaa tgctaaaaat acattaattt ctaaaacctg 1421

tgatgcccta agaagcatta agaatgaagg tgttgtacta atagaaacta agtacagaaa 1481

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tggtggagat ggccttctgg taactgaata ttaccttctg taggaaaagg tggaaaataa 1721

gcatttagaa ggttggttg aatgactctg tgctggcaaa aatgcttgaa acctctatat 1781

ttctttcggtt cataagaggt aaagggtcaaa tttttcaaca aaagtctttt aataacaaaa 1841

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gaatcaataa aaacaaacaa ggg 1924

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<211> 127

<212> PRT

<213> Homo sapiens

<400> 5

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Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly

20 25 30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val

35 40 45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val

50 55 60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
65 70 75 80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
85 90 95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe
100 105 110

Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser
115 120 125

<210> 6

<211> 702

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225).. (605)

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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacatttta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

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att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284

Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

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10

15

20

ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct 332

Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala

25

30

35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380

Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp

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45

50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428

Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro

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60

65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476

Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu

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75

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att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac 524

Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His

85

90

95

100

atg gag atg agt cct tgg ttc caa ttc atg ctg ttt atc ctg cag ctg 572

Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu

105

110

115

gac att gcc ttc aag cta aac aac caa atc agt taagtgtact ctctctcat 625

Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser

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gtaaaaatgg taatagt

702

<210> 7

<211> 233

<212> PRT

<213> Homo sapiens

<400> 7

Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile

1

5

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15

Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly

20

25

30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val

35

40

45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val

50	55	60
Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala		
65	70	75 80
Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile		
85	90	95
Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe		
100	105	110
Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu		
115	120	125
Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala		
130	135	140
Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu		
145	150	155 160
Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr		
165	170	175
Tyr Glu Cys Asp Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly		
180	185	190
Val Val Leu Glu Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser		
195	200	205

Gly Lys Ser His Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr

210

215

220

Pro Ser Gly Met Val Phe His Arg Val

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<210> 8

<211> 2409

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225).. (923)

<400> 8

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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcacct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284

Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

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ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct	332			
Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala				
25	30	35		
cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat	380			
Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp				
40	45	50		
gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc	428			
Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro				
55	60	65		
aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa	476			
Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu				
70	75	80		
att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac	524			
Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His				
85	90	95	100	
atg gag atg agt cct tgg ttc caa ttc atg ctg ttt atc ctg cag ctg	572			
Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu				
105	110	115		
gac att gcc ttc aag cta aac aac caa atc aga gaa aat gca gaa gtc	620			
Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val				
120	125	130		

tcc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg 668

Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp

135

140

145

act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc 716

Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe

150

155

160

aca tct ccc aag act cca gag cat gag ggc cgt tac tat gaa tgt gat 764

Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp

165

170

175

180

gtc ctt cct tac gcc cag cat ctt cat cat tat ggt gtg gta ttg gag 812

Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly Val Val Leu Glu

185

190

195

gag gat cac cat gat gtc ccg acc ccc agt gct tct gga aaa agt cat 860

Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser Gly Lys Ser His

200

205

210

ctt tgc cct tgg gat ttc cat gac ctt tat caa tat ccc agt gga atg 908

Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr Pro Ser Gly Met

215

220

225

gtt ttc cat cgg gtt tgactggacc tggatgctgc tgtttgggtga catccgacag 963

Val Phe His Arg Val

230

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gatcagcacg agcggaacca catcgcaggg tattggaagc aagtcggacc cattgccgtt 1083

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aatggcgatc tgggtgtcca tagtggggaa gaactccagc tcaccaccac tatcaccat 1623

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tgcagccact aatgcattgt gtatgataac aaaaactctg gtatgacaca ttttctgtga 1923
 tcattgttaa ttagtgacat agtaacatct gtagcagctg gttagtaaac ctcatgtggg 1983
 ggtgggggtgg ggggtgtattc cttgggggat ggtttgggcc gaatggggag tggaatattt 2043
 gacatttttc ctgttttaaa ttctaggata gattttaaca tcctttgcgg tcccagtcca 2103
 aggtaggctg gtgtcatagt cttctcactc ctaatccatg accactgttt ttttctatt 2163
 tatatcacca ggtagccac tgagttaata ttttaagttgt caatagataa gtgtccctgt 2223
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 tttgaaacca aatctgtgta tctaatacta accaatctgt tggatgtggg ttttaaaaaa 2343
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<210> 9
 <211> 198
 <212> PRT
 <213> Homo sapiens

<400> 9
 Met Ala Thr Leu Trp Gly Gly Leu Leu Arg Leu Gly Ser Leu Leu Ser

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20	25	30	
Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile Cys Pro Pro			
35	40	45	
Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn Ile Ser Gln Lys			
50	55	60	
Asp Cys Asp Cys Leu His Val Val Glu Pro Met Pro Val Arg Gly Pro			
65	70	75	80
Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu Cys Lys Tyr Glu Glu Arg			
85	90	95	
Ser Ser Val Thr Ile Lys Val Thr Ile Ile Ile Tyr Leu Ser Ile Leu			
100	105	110	
Gly Leu Leu Leu Leu Tyr Met Val Tyr Leu Thr Leu Val Glu Pro Ile			
115	120	125	
Leu Lys Arg Arg Leu Phe Gly His Ala Gln Leu Ile Gln Ser Asp Asp			
130	135	140	
Asp Ile Gly Asp His Gln Pro Phe Ala Asn Ala His Asp Val Leu Ala			
145	150	155	160

Arg Ser Arg Ser Arg Ala Asn Val Leu Asn Lys Val Glu Tyr Ala Gln

165

170

175

Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Ser Val Phe Asp

180

185

190

Arg His Val Val Leu Ser

195

<210> 10

<211> 1498

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (86).. (679)

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ctgtgggacc gctgggcccc cagcg atg gcg acc ctg tgg gga ggc ctt ctt 112

Met Ala Thr Leu Trp Gly Gly Leu Leu

1

5

cgg ctt ggc tcc ttg ctc agc ctg tcg tgc ctg gcg ctt tcc gtg ctg 160

Arg Leu Gly Ser Leu Leu Ser Leu Ser Cys Leu Ala Leu Ser Val Leu

10

15

20

25

ctg ctg gcg cag ctg tca gac gcc gcc aag aat ttc gag gat gtc aga 208

Leu Leu Ala Gln Leu Ser Asp Ala Ala Lys Asn Phe Glu Asp Val Arg

30 35 40

tgt aaa tgt atc tgc cct ccc tat aaa gaa aat tct ggg cat att tat 256

Cys Lys Cys Ile Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr

45 50 55

aat aag aac ata tct cag aaa gat tgt gat tgc ctt cat gtt gtg gag 304

Asn Lys Asn Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu

60 65 70

ccc atg cct gtg cgg ggg cct gat gta gaa gca tac tgt cta cgc tgt 352

Pro Met Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys

75 80 85

gaa tgc aaa tat gaa gaa aga agc tct gtc aca atc aag gtt acc att 400

Glu Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile

90 95 100 105

ata att tat ctc tcc att ttg ggc ctt cta ctt ctg tac atg gta tat 448

Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Leu Tyr Met Val Tyr

110 115 120

ctt act ctg gtt gag ccc ata ctg aag agg cgc ctc ttt gga cat gca 496

Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly His Ala

125 130 135

cag ttg ata cag agt gat gat gat att ggg gat cac cag cct ttt gca 544
 Gln Leu Ile Gln Ser Asp Asp Asp Ile Gly Asp His Gln Pro Phe Ala

140

145

150

aat gca cac gat gtg cta gcc cgc tcc cgc agt cga gcc aac gtg ctg 592
 Asn Ala His Asp Val Leu Ala Arg Ser Arg Ser Arg Ala Asn Val Leu

155

160

165

aac aag gta gaa tat gca cag cag cgc tgg aag ctt caa gtc caa gag 640
 Asn Lys Val Glu Tyr Ala Gln Gln Arg Trp Lys Leu Gln Val Gln Glu

170

175

180

185

cag cga aag tct gtc ttt gac cgg cat gtt gtc ctc agc taattgggaa 689
 Gln Arg Lys Ser Val Phe Asp Arg His Val Val Leu Ser

190

195

ttgaattcaa ggtgactaga aagaaacagg cagacaactg gaaagaactg actgggtttt 749

gctgggttttc attttaatac cttgttgatt tcaccaactg ttgctggaag attcaaaact 809

ggaagcaaaa acttgcttga tttttttttc ttgttaacgt aataatagag acatttttaa 869

aagcacacag ctcaaagtca gccataaagt cttttcctat ttgtgacttt tactaataaa 929

aataaatctg cctgtaaatt atcttgaagt cctttacctg gaacaagcac tctctttttc 989

accacatagt ttaacttga ctttcaagat aattttcagg gtttttggtg ttgttgtttt 1049

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<210> 11

<211> 221

<212> PRT

<213> Homo sapiens

<400> 11

Met Ala Leu Ala Leu Ala Ala Leu Ala Ala Val Glu Pro Ala Cys Gly

1 5 10 15

Ser Arg Tyr Gln Gln Leu Gln Asn Glu Glu Glu Ser Gly Glu Pro Glu

20 25 30

Gln Ala Ala Gly Asp Ala Pro Pro Pro Tyr Ser Ser Ile Ser Ala Glu

35	40	45
Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe Pro Lys Pro		
50	55	60
Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp Glu Ala Glu		
65	70	75 80
Arg Thr Lys Ala Glu Ala Thr Ile Pro Leu Val Pro Gly Arg Asp Glu		
85	90	95
Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln Leu Arg Ile		
100	105	110
Gly Asn Asp Gly Ile Phe Met Leu Thr Phe Phe Met Ala Phe Leu Phe		
115	120	125
Asn Trp Ile Gly Phe Phe Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala		
130	135	140
Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp		
145	150	155 160
Ile Leu Ile Val Arg Phe Ser Thr Tyr Phe Pro Gly Tyr Phe Asp Gly		
165	170	175
Gln Tyr Trp Leu Trp Trp Val Phe Leu Val Leu Gly Phe Leu Leu Phe		
180	185	190

Leu Arg Gly Phe Ile Asn Tyr Ala Lys Val Arg Lys Met Pro Glu Thr

195

200

205

Phe Ser Asn Leu Pro Arg Thr Arg Val Leu Phe Ile Tyr

210

215

220

<210> 12

<211> 1864

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (153)..(815)

<400> 12

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gctcgctctg cttccctgct gccggtgcg cc atg gcg ttg gcg ttg gcg gcg 173

Met Ala Leu Ala Leu Ala Ala

1

5

ctg gcg gcg gtc gag ccg gcc tgc ggc agc cgg tac cag cag ttg cag 221

Leu Ala Ala Val Glu Pro Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln

10

15

20

aat gaa gaa gag tct gga gaa cct gaa cag gct gca ggt gat gct cct	269
Asn Glu Glu Glu Ser Gly Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro	
25 30 35	
cca cct tac agc agc att tct gca gag agc gca gca tat ttt gac tac	317
Pro Pro Tyr Ser Ser Ile Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr	
40 45 50 55	
aag gat gag tct ggg ttt cca aag ccc cca tct tac aat gta gct aca	365
Lys Asp Glu Ser Gly Phe Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr	
60 65 70	
aca ctg ccc agt tat gat gaa gcg gag agg acc aag gct gaa gct act	413
Thr Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr	
75 80 85	
atc cct ttg gtt cct ggg aga gat gag gat ttt gtg ggt cgg gat gat	461
Ile Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp	
90 95 100	
ttt gat gat gct gac cag ctg agg ata gga aat gat ggg att ttc atg	509
Phe Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met	
105 110 115	
tta act ttt ttc atg gca ttc ctc ttt aac tgg att ggg ttt ttc ctg	557
Leu Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu	
120 125 130 135	

tct ttt tgc ctg acc act tca gct gca gga agg tat ggg gcc att tca 605
 Ser Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser
 140 145 150

gga ttt ggt ctc tct cta att aaa tgg atc ctg att gtc agg ttt tcc 653
 Gly Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser
 155 160 165

acc tat ttc cct gga tat ttt gat ggt cag tac tgg ctc tgg tgg gtg 701
 Thr Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val
 170 175 180

ttc ctt gtt tta ggc ttt ctc ctg ttt ctc aga gga ttt atc aat tat 749
 Phe Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr
 185 190 195

gca aaa gtt cgg aag atg cca gaa act ttc tca aat ctc ccc agg acc 797
 Ala Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr
 200 205 210 215

aga gtt ctc ttt att tat taaagatggt ttctggcaaa ggccttcctg 845
 Arg Val Leu Phe Ile Tyr
 220

catttatgaa ttctctctca agaagcaaga gaacacctgc aggaagtga tcaagatgca 905

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<210> 13

<211> 242

<212> PRT

<213> Homo sapiens

<400> 13

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn

1 5 10 15

Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser

20 25 30

Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu

35 40 45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val

50 55 60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro

65 70 75 80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu

85 90 95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln

100 105 110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala

115	120	125
Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe		
130	135	140
Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile		
145	150	155 160
Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu		
165	170	175
Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr		
180	185	190
Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu		
195	200	205
Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg		
210	215	220
Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe		
225	230	235 240
Leu Leu		

<210> 14

<211> 2324

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (13)..(738)

<400> 14

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Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val

1 5 10

ctt ctt aat gaa gag gat aac tca gaa tca tcg gct ata gag cag cca 99

Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro

15 20 25

cct act tca aac cca gca ccg cag att gtg cag gct gcg tct tca gca 147

Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala

30 35 40 45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195

Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr

50 55 60

gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat 243

Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr

65 70 75

ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat 291

Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp

80

85

90

gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa 339

Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu

95

100

105

aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc 387

Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe

110

115

120

125

agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg 435

Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu

130

135

140

gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc 483

Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser

145

150

155

ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga 531

Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly

160

165

170

ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat 579

Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp

175

180

185

tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt 627

Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe

190	195	200	205	
ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta				675
Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu				
	210	215	220	
aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg				723
Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg				
	225	230	235	
tat ttc ttc tta ttg tagagactgc atcaaccgga cattcctttc ttataccaat				778
Tyr Phe Phe Leu Leu				
	240			
gtgaaatttc cagatcatct gtaaacctac aactttaata gaagactact aataacagaa				838
gacaaattag tgaagaaaag acggagtttc gaaattgaat ggcagggtgg tttttgctta				898
caagccattt ctgttcattc ttaaagtatc tatatttcat ttgttttgca catatgcata				958
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tccagtcaca tttggttaat cagtgtttga tataattgaa agagttgagt ggataaacag				1078
tcttccagct tgtaaatgcc attgacttct gacctgacat ttagtataat aaaaatgaaa				1138
ttcttaacca tgtcaaatga tttagtttct ggctcttaga ctcatctggc agttctacac				1198
atgaaacatc ttttggttata tagggtgtat tgaaacctgc agtgctgatt attagaaagg				1258

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actaatttta aattaagtga actaaatata tatgtgtata tgtatacaca tatatataca 1438

cacacacata tatatatatta gaaacgtgag tgttaaagat agaatttggt ttaggacaaa 1498

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aagagatcct gcaggaagag attgtattag atattatatt tatttcattt aagataattt 1678

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ataaaatcct gtactatgaa tagcttcttg ctttatgact ttaggattaa cttgtaaaaa 1858

acatatcctg aactgagata tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg 1918

gcatatagga ctgtggggtc tgtgtgtgta gtgagagtgt gtagccacta ttataactgg 1978

aatttaattt acattcataa actactatat tccccatctt gcaaatacatt ttatgtctca 2038

tctgtttttc ctttcgggta tatcttttgt tttgaatacc aacatttaaa atgatgggtat 2098

tttatctttt aaacttaaaa attattttaat acagctatat ggaccttata aaattgattt 2158

cttattttatt attagacatt actactaaaa ggtacatcta actattcagg gacatttttc 2218

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<210> 15

<211> 242

<212> PRT

<213> Homo sapiens

<400> 15

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn

1 5 10 15

Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser

20 25 30

Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu

35 40 45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val

50 55 60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro

65 70 75 80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu

85

90

95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln

100

105

110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala

115

120

125

Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe

130

135

140

Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile

145

150

155

160

Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu

165

170

175

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr

180

185

190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu

195

200

205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg

210

215

220

Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe

225

230

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240

Leu Leu

<210> 16

<211> 2324

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (13).. (738)

<400> 16

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Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val

1

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ctt ctt aat gaa gag gat aac tca gaa tca tcg gct ata gag cag cca 99

Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro

15

20

25

cct act tca aac cca gca ccg cag att gtg cag gct gtg tct tca gca 147

Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala

30

35

40

45

cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act 195

Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr

50

55

60

gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat 243

Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr

65

70

75

ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat 291

Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp

80

85

90

gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa 339

Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu

95

100

105

aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc 387

Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe

110

115

120

125

agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg 435

Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu

130

135

140

gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc 483

Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser

145

150

155

ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga 531

Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly

160	165	170	
ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat	579		
Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp			
175	180	185	
tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt	627		
Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe			
190	195	200	205
ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta	675		
Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu			
210	215	220	
aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg	723		
Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg			
225	230	235	
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Tyr Phe Phe Leu Leu			
240			
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gacaaattag tgaagaaaag acggagtttc gaaattgaat ggcagggtgg tttttgctta	898		
caagccattt ctgttcattc ttttaagtatc tatattttcat ttgttttgca catatgcata	958		
tgtgcccatt taagatatatt gcataactt gatagaaacc ataaagttgt agcagttaag	1018		

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taaccatgca taacttactt tctgcaatgt tttcttagaa attgtgtcca gatagctttc 1378

actaatttta aattaagtga actaaatata tatgtgtata tgtatacaca tatatataca 1438

cacacacata tatatattht gaaacgtgag tgttaaagat agaatttgtht ttaggacaaa 1498

ttttaagaaa atgtgggaat accaaatgtht ctttataaga aaaataaatt ttattthttag 1558

ggacatacta gttttaggga ttttcagatg ggaagctgca tttttaggat tgcccatctt 1618

aagagatctt gcaggaagag attgtattag atattatatt tatttcattt aagataattt 1678

tcaaagttaa ttttctaaat aagataattht tcatttgtht ttgtcttht aaaggccaat 1738

aaaatatctt tcagtatcat tgtaataatt ttttagagtht taatttgtaa agcttagcaa 1798

ataaaatctt gtactatgaa tagcttcttg ctttatgact ttaggattaa cttgtaaaaa 1858

acatatacctg aactgagata tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg 1918
 gcatatagga ctgtggggtc tgtgtgtgta gtgagagtgt gtagccacta ttataactgg 1978
 aatttaattt acattcataa actactatat ttcccatctt gcaaatcatt ttatgtctca 2038
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<210> 17

<211> 336

<212> PRT

<213> Homo sapiens

<400> 17

Met Ala Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met

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Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr

20

25

30

Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu
35 40 45

Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro
50 55 60

Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly
65 70 75 80

Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp
85 90 95

His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu
100 105 110

Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro
115 120 125

Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr
130 135 140

Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr
145 150 155 160

Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro
165 170 175

Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala
180 185 190

Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile
195 200 205

Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln
210 215 220

Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala
225 230 235 240

Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn
245 250 255

Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu
260 265 270

Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr
275 280 285

Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu
290 295 300

Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met
305 310 315 320

Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
325 330 335

<210> 18

<211> 2636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53)..(1060)

<400> 18

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Met Ala

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cgc cgg cgg agc cag cga gtc tgc gcg agc ggt ccg agc atg ctc aat 106

Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn

5

10

15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154

Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala

20

25

30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202

Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro

35

40

45

50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250

Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala

55

60

65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac 298
 Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp

70 75 80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346
 Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His

85 90 95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394
 Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn

100 105 110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg 442
 Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro

115 120 125 130

cag att gtg cag gct gtg tct tca gca cca gca ctt gaa act gac tct 490
 Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser

135 140 145

tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca 538
 Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser

150 155 160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc 586
 Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser

165 170 175

gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct 634
Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala
180 185 190

gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag 682
Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu
195 200 205 210

gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga 730
Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg
215 220 225

gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att 778
Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile
230 235 240

ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata 826
Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile
245 250 255

gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa 874
Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys
260 265 270

tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat 922
Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn
275 280 285 290

gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt 970

Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu

295

300

305

ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa 1018

Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu

310

315

320

agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg 1060

Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu

325

330

335

tagagactgc atcaaccgga cattcctttc ttataccaat gtgaaatttc cagatcatct 1120

gtaaacctac aactttaata gaagactact aataacagaa gacaaattag tgaagaaaag 1180

acggagtttc gaaattgaat ggcagggtgg tttttgctta caagccattt ctgttcattc 1240

tttaagtatc tatatttcat ttgttttgca catatgcata tgtgccatt taagatattt 1300

gcatatactt gatagaaacc ataaagttgt agcagttaag tccagtcaca tttggttaat 1360

cagtgtttga tataattgaa agagttgagt ggataaacag tcttcagct tgtaaagcc 1420

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actaaatata tatgtgtata tgtatacaca tatatatata cacacacata tatatattta 1780

gaaacgtgag tgtaaagat agaatttggt ttaggacaaa ttttaagaaa atgtgggaat 1840

accaaattgc ctttataaga aaaataaatt ttgttttaag ggacatacca gtttaggga 1900

tttcagatg ggaagctgca ttttaggat tgccatctt aagagatctt gcaggaagag 1960

attgtattag atattatatt tatttcattt aagataattt tcaaagttaa tttctaaat 2020

aagataattc tcatttgtgt ttgtctttta aaaggccaat aaaatatctt tcagtatcat 2080

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tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg gcatatagga ctgtggggtc 2260

tgtgtgtgta gtgagagtgt gtagccacta ttataactgg aatttaattt acattcataa 2320

actactatat ttcccatctt gcaaattcatt ttatgtctca tctgtttttc ctttcggtta 2380

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attatttaat acagctatat ggaccttata aaattgattt cttatttatt attagacatt 2500

actactaaaa ggtacatcta actattcagg gacatTTTTc catttccaaa aaataaaatt 2560

tattatgctt tataacctct tctgtatTTT ctaatTTTT cattgtcttt gataaataaa 2620

acagTTTTgt tttgct 2636

<210> 19

<211> 336

<212> PRT

<213> Homo sapiens

<400> 19

Met Ala Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met

1 5 10 15

Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr

20 25 30

Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu

35 40 45

Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro

50 55 60

Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly

65 70 75 80

Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp
85 90 95

His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu
100 105 110

Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro
115 120 125

Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr
130 135 140

Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr
145 150 155 160

Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro
165 170 175

Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala
180 185 190

Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile
195 200 205

Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln
210 215 220

Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala
225 230 235 240

Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn
245 250 255

Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu
260 265 270

Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr
275 280 285

Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu
290 295 300

Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met
305 310 315 320

Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
325 330 335

<210> 20

<211> 2636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53)..(1060)

<400> 20

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Met Ala

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cgc cgg cgg agc cag cga gtc tgc gcg agc ggt ccg agc atg ctc aat 106

Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn

5

10

15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg 154

Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala

20

25

30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg 202

Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro

35

40

45

50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg 250

Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala

55

60

65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac 298

Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp

70

75

80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac 346

Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His

85

90

95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac 394
 Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn
 100 105 110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg 442
 Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro
 115 120 125 130

cag att gtg cag gct gcg tct tca gca cca gca ctt gaa act gac tct 490
 Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser
 135 140 145

tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca 538
 Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser
 150 155 160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc 586
 Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Tyr Ser
 165 170 175

gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct 634
 Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala
 180 185 190

gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag 682
 Ala Ala Met Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu
 195 200 205 210

gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga 730

Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg	
215	220
225	
gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att	778
Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile	
230	235
240	
ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata	826
Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile	
245	250
255	
gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa	874
Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys	
260	265
270	
tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat	922
Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn	
275	280
285	290
gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt	970
Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu	
295	300
305	
ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa	1018
Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu	
310	315
320	
agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg	1060
Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu	

tagagactgc atcaaccga cattcctttc ttataccaat gtgaaatttc cagatcatct 1120

gtaaacctac aactttaata gaagactact aataacagaa gacaaattag tgaagaaaag 1180

acggagtttc gaaattgaat ggcagggtgg tttttgctta caagccattt ctgttcattc 1240

tttaagtatc tatatttcatt ttgttttgca catatgcata tgtgcccatt taagatattt 1300

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cagtgtttga tataattgaa agagttgagt ggataaacag tcttcagct tgtaaagcc 1420

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tgatatttac attattattt aggaaaactc ttctgtaaa taaccatgca taacttactt 1660

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actaaatata tatgtgtata tgtatacaca tatatataca cacacacata tatatattta 1780

gaaacgtgag tgtaaagat agaatttggt ttaggacaaa ttttaagaaa atgtgggaat 1840

accaaagtc ctttataaga aaaataaatt ttgttttaag ggacatacca gttttaggga 1900

ttttcagatg ggaagctgca tttttaggat tgcccatcctt aagagatcctt gcaggaagag 1960
 attgtattag atattatatt tatttcattt aagataattt tcaaagttaa ttttctaaat 2020
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 actactaaaa ggtacatcta actattcagg gacatttttc catttccaaa aaataaaaatt 2560
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<211> 76

<212> PRT

<213> Homo sapiens

<400> 21

Met Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr

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Lys Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val

20 25 30

Ser Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn

35 40 45

Lys Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr

50 55 60

Lys Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp

65 70 75

<210> 22

<211> 1085

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (176)..(403)

<400> 22

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cggcctccgc ggtgcctgcc ttcgctctca ggttgaggag ctcaagcttg ggaaa atg 178

Met

1

gtg tgc att cct tgt atc gtc att cca gtt ctg ctc tgg atc tac aaa 226

Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr Lys

5

10

15

aaa ttc ctg gag cca tat ata tac cct ctg gtt tcc ccc ttc gtt agt 274

Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val Ser

20

25

30

cgt ata tgg cct aag aaa gca ata caa gaa tcc aat gat aca aac aaa 322

Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn Lys

35

40

45

ggc aaa gta aac ttt aag ggt gca gac atg aat gga tta cca aca aaa 370

Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr Lys

50

55

60

65

gga cca aca gaa atc tgt gat aaa aag aaa gac taaagaaatt ttcctaaagg 423

Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp

70

75

accccatcat ttaaaaaatg gacctgataa tatgaagcat cttccttgta attgtctctg 483
 acctttttat ctgagaccgg aattcaggat aggagtctag atatttacct gataactaatc 543
 aggaaatata tgatatccgt atttaaaatg tagttagtta tatttaatga cctcattcct 603
 aagttccttt ttcgttaatg tagctttcat ttctgttatt gctgtttgaa taatatgatt 663
 aaatagaagg tttgtgccag tagacattat gttactaaat cagcacttta aaatccttgg 723
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 gatagggaaa aggggggaaac ttctttgaaa aatgaaacat ctgttacatt aatgtctaatt 1023
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 tt 1085

<210> 23
 <211> 84
 <212> PRT

<213> Homo sapiens

<400> 23

Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu
1 5 10 15

Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val
20 25 30

Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile
35 40 45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr Trp
50 55 60

Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His Ser
65 70 75 80

Leu Ser Gly Leu

<210> 24

<211> 1593

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (65).. (316)

<400> 24

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cgcc atg gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc 109

Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile

1

5

10

15

ctg ccg gaa att cag aag cca gag agg aag att cag ttt aag gag aaa 157

Leu Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys

20

25

30

gtg ctg tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag 205

Val Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln

35

40

45

att ccc ctg ttt ggg atc atg tct tca gat tca gct gac cct ttc tat 253

Ile Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr

50

55

60

tgg atg aga gtg att cta gcc tct aac aga ggc aca ttg atg gag cac 301

Trp Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His

65

70

75

tct ctc tct ggc ctt tagggagtcc cctcttagga caggcactgc ccagcagcaa 356

Ser Leu Ser Gly Leu

80

gggcagcaga gttgggtgct aagatcctga ggagctcgag gtttcgagct ggcttttagac 416

attggtggga ccaaggatgt tttgcaggat gccctgatcc taagaagggg gcctgggggt 476

gcgtgcagcc tgtcggggag accccactct gtgcacctat tggetcttct agctgactct 536

tctcgttggg cttagagtct gcctgtttct gctagctccg tgtttagtcc acttgggtca 596

tcagctctgc caagctgagc ctggccaage taggtggaca gacccttgca gtgatgtccg 656

tttgtccaga ttctgccagt catcactgga cacgtctcct cgcagctgcc ctagcaaggg 716

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caccttctgg gctgaagatc acccagctgt gttcagaatt ttcttactgt gcttaggact 836

gcacgcaagt gagcagacac caccgacttc ctttctgcgt caccagtgtc gtcagcagag 896

agaggacagc acaggctcaa gtttggtagt gaagtcaggt tcgggggtgca tgggctgtgg 956

tggtggtgat cagttgctcc agtgtttgaa ataagaagac tcatgtttat gtctggaata 1016

agttctgttt gtgctgacag gtgaccttgc tggcagtgt agccaggaaa cagagtgacc 1076

aagggacaag aagggacttg cctaaagcca cccagcaact cagcagcaga accaagatgg 1136

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accagtcct gagcagggga gaggtcttg agacctgatg ccttcctacc cacatggttc 1256

tcccactgcc ctgtctgctc tgctgctaca gaggggcagg gcctccccc a gcccacgctt 1316

aggaatgctt ggcctctggc aggcaggcag ctgtacccaa gctgggtgggc agggggctgg 1376

aaggcaccag gcctcaggag gagccccata gtcccgcctg cagcctgtaa ccatcggtg 1436

ggccctgcaa ggcccacact cacgccctgt gggatgatggt cacggtgggt ggggtgggggc 1496

tgaccccagc ttccagggga ctgtcactgt ggacgccaaa atggcataac tgagataagg 1556

tgaataagtg acaaataaag ccagtttttt acaaggt 1593

<210> 25

<211> 179

<212> PRT

<213> Homo sapiens

<400> 25

Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu

1 5 10 15

Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val

20 25 30

Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile

35 40 45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala
50 55 60

Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys
65 70 75 80

Thr Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln
85 90 95

Leu Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met
100 105 110

Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly
115 120 125

Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile
130 135 140

Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr
145 150 155 160

Phe Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala
165 170 175

Leu Leu Phe

<211> 1820

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (114).. (650)

<400> 26

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acgcgggagca gagctgagct gaagcgggac ccggagcccg agcagccgcc gcc atg 116

Met

1

gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc ctg ccg 164

Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu Pro

5

10

15

gaa att cag aag cca gag agg aag att cag ttt aag gag aaa gtg ctg 212

Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val Leu

20

25

30

tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag att ccc 260

Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile Pro

35

40

45

ctg ttt ggg atc atg tct tca gat tca gct gac ccg gtc cat gca gtt 308

Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala Val

50	55	60	65	
gta tac ata gtg ttc atg ctg ggc tcc tgt gca ttc ttc tcc aaa acg				356
Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys Thr				
	70	75	80	
tgg att gag gtc tca ggt tcc tct gcc aaa gat gtt gca aag cag ctg				404
Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln Leu				
	85	90	95	
aag gag cag cag atg gtg atg aga ggc cac cga gag acc tcc atg gtc				452
Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met Val				
	100	105	110	
cat gaa ctc aac cgg tac atc ccc aca gcc gcg gcc ttt ggt ggg ctg				500
His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly Leu				
	115	120	125	
tgc atc ggg gcc ctc tcg gtc ctg gct gac ttc cta ggc gcc att ggg				548
Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile Gly				
130	135	140	145	
tct gga acc ggg atc ctg ctc gca gtc aca atc atc tac cag tac ttt				596
Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr Phe				
	150	155	160	
gag atc ttc gtt aag gag caa agc gag gtt ggc agc atg ggg gcc ctg				644
Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala Leu				
	165	170	175	

ctc ttc tgagcccgtc tcccggacag gttgaggaag ctgctccaga agcgcctcgg 700

Leu Phe

aaggggagct ctcatcatgg cgcgtgctgc tgcggcatat ggacttttaa taatgttttt 760

gaatttcgta ttctttcatt ccactgtgta aagtgctaga cattttccaa tttaaaattt 820

tgctttttat cctggcactg gcaaaaagaa ctgtgaaagt gaatttattc agccgactgc 880

cagagaagtg ggaatggtat aggattgtcc ccaagtgtcc atgtaacttt tgttttaacc 940

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aatttctcac tctggttgga agcacaaaca ctgaaatgtc tacgtttcat tttggcagta 1060

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gaccaaggga caagaaggga cttgcctaaa gccacccagc aactcagcag cagaaccaag 1360

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aagtgata agtgacaaat aaagccagtt tttacaagg 1820

<210> 27

<211> 279

<212> PRT

<213> Homo sapiens

<400> 27

Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp

1 5 10 15

Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr

20 25 30

Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg

35 40 45

Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val
50 55 60

Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe
65 70 75 80

Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val
85 90 95

Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp
100 105 110

Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe
115 120 125

Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His
130 135 140

His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro
145 150 155 160

Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val
165 170 175

Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln
180 185 190

Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln
195 200 205

Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser
210 215 220

Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly
225 230 235 240

Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr
245 250 255

Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly
260 265 270

Ile Ala Lys Val Lys Ala Asn
275

<210> 28

<211> 1472

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119).. (955)

<400> 28

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tgctccctcc gagegctccg ccgttgcccg cctggcccct acggagtcct tagccagg 118

atg gag gct gtt gtg aac ttg tac caa gag gtg atg aag cac gca gat 166

Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp

1 5 10 15

ccc cgg atc cag ggc tac cct ctg atg ggg tcc ccc ttg cta atg acc 214

Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr

20 25 30

tcc att ctc ctg acc tac gtg tac ttc gtt ctc tca ctt ggg cct cgc 262

Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg

35 40 45

atc atg gct aat cgg aag ccc ttc cag ctc cgt ggc ttc atg att gtc 310

Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val

50 55 60

tac aac ttc tca ctg gtg gca ctc tcc ctc tac att gtc tat gag ttc 358

Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe

65 70 75 80

ctg atg tcg ggc tgg ctg agc acc tat acc tgg cgc tgt gac cct gtg 406

Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val

85 90 95

gac tat tcc aac agc cct gag gca ctt agg atg gtt cgg gtg gcc tgg 454

Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp

100 105 110

ctc ttc ctc ttc tcc aag ttc att gag ctg atg gac aca gtg atc ttt 502
 Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe

115

120

125

att ctc cga aag aaa gac ggg cag gtg acc ttc cta cat gtc ttc cat 550
 Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His

130

135

140

cac tct gtg ctt ccc tgg agc tgg tgg tgg ggg gta aag att gcc ccg 598
 His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro

145

150

155

160

gga gga atg ggc tct ttc cat gcc atg ata aac tct tcc gtg cat gtc 646
 Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val

165

170

175

ata atg tac ctg tac tac gga tta tct gcc ttt ggc cct gtg gca caa 694
 Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln

180

185

190

ccc tac ctt tgg tgg aaa aag cac atg aca gcc att cag ctg atc cag 742
 Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln

195

200

205

ttt gtc ctg gtc tca ctg cac atc tcc cag tac tac ttt atg tcc agc 790
 Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser

210

215

220

tgt aac tac cag tac cca gtc att att cac ctc atc tgg atg tat ggc 838
 Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly
 225 230 235 240

acc atc ttc ttc atg ctg ttc tcc aac ttc tgg tat cac tct tat acc 886
 Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr
 245 250 255

aag ggc aag cgg ctg ccc cgt gca ctt cag caa aat gga gct cca ggt 934
 Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly
 260 265 270

att gcc aag gtc aag gcc aac tgagaagcat ggcctagata ggcgcccacc 985
 Ile Ala Lys Val Lys Ala Asn
 275

taagtgcctc aggactgcac cttagggcag tgtccgtcag tgccctctcc acctacacct 1045

gtgaccaagg cttatgtggt caggactgag caggggactg gccctcccct cccacagct 1105

gctctacagg gaccacgget ttggttcctc acccacttcc cccgggcagc tccagggatg 1165

tggcctcatt gctgtctgcc actccagagc tgggggctaa aagggtgta cagttatttc 1225

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ggaaacc

1472

<210> 29

<211> 137

<212> PRT

<213> Homo sapiens

<400> 29

Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu

1 5 10 15

Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu

20 25 30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser

35 40 45

Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro

50 55 60

Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln

65 70 75 80

Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr

85 90 95

Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly

100

105

110

Gly Ala Ala Ala Pro Tyr Pro Ala Ser Gln Pro Pro Tyr Asn Pro Ala

115

120

125

Tyr Met Asp Ala Pro Lys Ala Ala Leu

130

135

<210> 30

<211> 1788

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (145).. (555)

<400> 30

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ggaaattgaa actgagtggc ccacgatggg aagaggggaa agcccagggg tacaggaggc 120

ctctgggtga aggcagaggc taac atg ggg ttc gga gcg acc ttg gcc gtt 171

Met Gly Phe Gly Ala Thr Leu Ala Val

1

5

ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc ttc 219
 Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys Phe
 10 15 20 25

acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt ccg 267
 Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg Pro
 30 35 40

gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat cct 315
 Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr Pro
 45 50 55

cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag ggc 363
 Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln Gly
 60 65 70

tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac cca 411
 Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr Pro
 75 80 85

atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg gcc 459
 Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro Ala
 90 95 100 105

tac cac gag acc ctg gct gga gga gca gcc gcg ccc tac ccc gcc agc 507
 Tyr His Glu Thr Leu Ala Gly Gly Ala Ala Ala Pro Tyr Pro Ala Ser
 110 115 120

cag cct cct tac aac ccg gcc tac atg gat gcc ccg aag gcg gcc ctc 555

Gln Pro Pro Tyr Asn Pro Ala Tyr Met Asp Ala Pro Lys Ala Ala Leu

125

130

135

tgagcattcc ctggcctctc tggctgccac ttggttatgt tgtgtgtgtg cgtgagtgg 615

gtgcaggcgc ggttccttac gcccattgtg tgctgtgtgt gtccaggcac ggttccttac 675

gcccattgtg tgctgtgtgt gtcctgcctg tatatgtggc ttcctctgat gctgacaagg 735

tggggaacaa tccttgccag agtgggctgg gaccagactt tgttctcttc ctcacctgaa 795

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gaggtggccc ctgagaggtg ggggcctctc cagggcacat ctggagttct tctccagctt 915

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<210> 31

<211> 118

<212> PRT

<213> Homo sapiens

<400> 31

Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu

1 5 10 15

Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu

20 25 30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser
35 40 45

Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro
50 55 60

Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln
65 70 75 80

Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr
85 90 95

Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly
100 105 110

Glu Cys Pro Cys Gln Leu
115

<210> 32

<211> 1908

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91).. (444)

<400> 32

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 ggaggcctct ggggaaggc agaggctaac atg ggg ttc gga gcg acc ttg gcc 114
 Met Gly Phe Gly Ala Thr Leu Ala
 1 5

 gtt ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc 162
 Val Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys
 10 15 20

 ttc acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt 210
 Phe Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg
 25 30 35 40

 ccg gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat 258
 Pro Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr
 45 50 55

 cct cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag 306
 Pro Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln
 60 65 70

 ggc tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac 354
 Gly Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr
 75 80 85

 cca atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg 402
 Pro Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro
 90 95 100

gcc tac cac gag acc ctg gct ggt gag tgc ccc tgc caa ctc 444

Ala Tyr His Glu Thr Leu Ala Gly Glu Cys Pro Cys Gln Leu

105

110

115

tagccctgcc cgacttcccg agtctctgcc agcatccctc gggcacccat cccaaactac 504

atcactcaac aggccctctgc ccctttctgc ttgcctgcc ctcacacggc agcccacccat 564

gtcacagcc aaccagggtc ctctctgctt tcaggaggag cagccgcgcc ctaccccgcc 624

agccagcctc cttacaaccc ggcctacatg gatgccccga aggcggccct ctgagcattc 684

cctggcctct ctggctgcc cttggttatg ttgtgtgtgt gcgtgagtgg tgtgcaggcg 744

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gtgctgtgtg tgtcctgcct gtatatgtgg cttcctctga tgctgacaag gtggggaaca 864

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 tttataataa atgcaatcgt ttgg 1908

<210> 33

<211> 168

<212> PRT

<213> Homo sapiens

<400> 33

Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro Val Gln
1 5 10 15

Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro Gln Ala
20 25 30

Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr Arg Pro
35 40 45

Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser Ala Ala
50 55 60

Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val Ala Val
65 70 75 80

Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val Gly Pro
85 90 95

Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr Asp Ala
100 105 110

Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro Pro Pro
115 120 125

Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met Gln Gly

130	135	140	
Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met Gly Gly			
145	150	155	160

Ser Asp Gly Gly Tyr Thr Ile Trp

165

<210> 34

<211> 1897

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70).. (573)

<400> 34

ctccgaacag gaagaggacg aaaaaaataa ccgtccgcga cgccgagaca aaccggaccc 60

gcaaccacc atg aac agc aaa ggt caa tat cca aca cag cca acc tac cct 111

Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro

1

5

10

gtg cag cct cct ggg aat cca gta tac cct cag acc ttg cat ctt cct 159

Val Gln Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro

15

20

25

30

cag gct cca ccc tat acc gat gct cca cct gcc tac tca gag ctc tat 207
 Gln Ala Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr
 35 40 45

cgt ccg agc ttt gtg cac cca ggg gct gcc aca gtc ccc acc atg tca 255
 Arg Pro Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser
 50 55 60

gcc gca ttt cct gga gcc tct ctg tat ctt ccc atg gcc cag tct gtg 303
 Ala Ala Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val
 65 70 75

gct gtt ggg cct tta ggt tcc aca atc ccc atg gct tat tat cca gtc 351
 Ala Val Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val
 80 85 90

ggt ccc atc tat cca cct ggc tcc aca gtg ctg gtg gaa gga ggg tat 399
 Gly Pro Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr
 95 100 105 110

gat gca ggt gcc aga ttt gga gct ggg gct act gct ggc aac att cct 447
 Asp Ala Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro
 115 120 125

cct cca cct cct gga tgc cct ccc aat gct gct cag ctt gca gtc atg 495
 Pro Pro Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met
 130 135 140

cag gga gcc aac gtc ctc gta act cag cgg aag ggg aac ttc ttc atg 543

Gln Gly Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met

145

150

155

ggt ggt tca gat ggt ggc tac acc atc tgg tgaggaacca aggccacctc 593

Gly Gly Ser Asp Gly Gly Tyr Thr Ile Trp

160

165

tgtgccggga aagacatcac ataccttcag cactttctcac aatgtaactg ctttagtcat 653

attaacctga agttgcagtt tagacacatg ttgttggggg gtctttcttg tgcccaaact 713

ttcaggcact tttcaaattt aataaggaac catgtaatgg tagcagtacc tccctaaagc 773

at ttgaggt aggggaggta tccattcata aaatgaatgt gggatgaagcc gccctaagga 833

ttttccttta atttctctgg agtaatactg taccatactg gtctttgctt ttagtaataa 893

aacatcaaat taggtttgga gggaactttg atcttcctaa gaattaaagt tgccaaatta 953

ttctgattgg tctttaatct cctttaagtc ttgatatat attacttggt ataaatggaa 1013

cgcattagtt gtctgccttt tcctttccat cccttgcccc acccatccca tctccaaccc 1073

tagtcttcca tttcctcccg ccagtctcca ttgaatcaat ggtgcaggac agaaagccag 1133

tcagactaat ttccttcttt cctcgcaact ctccccactc gtcattcttt aactagtgtt 1193

tcacaaggat cctctgaaac cctctctgtg cccaagtac agatgccatt acttctgctt 1253

tcgtatctcc tcaggcaaaa gtggagggtg ccttatgggc cctcctcata ggttgtctct 1313
 gcatacaga acctaacca aatttgcttt ggtgccagaa aaactgagct atgtttgaac 1373
 aaagatgtcg tgcaaactgt actgtgaaca acagttggtt taaaatatga ggggcaagga 1433
 ggaggatgca tttcaaaagc ttgattgatg tgttcagagc taaattaaga ggagttttca 1493
 gatcaaaaac tggttaccat tttttgtcag agtgtctgat gcggccactc attcggtccc 1553
 ccagaattcc tagactgggt taatagggtc atattgtgaa tgtctcacta caaaatgact 1613
 tgagtccagt gaaatctcat tagggtttaa gaatatttca gggatcctta atgttttgat 1673
 ttttgtttcc tgaaattgga ttttatttta ttttatctta taatttcagt tcatctaaat 1733
 tgtgtgttct gtacatgtga tgtttgactg taccattgac tgttatggaa gttcagcggt 1793
 gtatgtctct ctctacactg tgggtgcactt aacttgtgga atttttatac taaaaatgta 1853
 gaataaagac tattttgaag atttgaataa agtgatgaag ttgc 1897

<210> 35

<211> 455

<212> PRT

<213> Homo sapiens

<400> 35

Met Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu
1 5 10 15

Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp
20 25 30

Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe
35 40 45

Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly
50 55 60

Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys
65 70 75 80

Val Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr
85 90 95

Phe Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe
100 105 110

Ser Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly
115 120 125

Asp Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu
130 135 140

Gln Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu
145 150 155 160

Leu Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr
165 170 175

Phe Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg
180 185 190

Leu Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala
195 200 205

Met Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro
210 215 220

Ser Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly
225 230 235 240

Ser Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu
245 250 255

Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys
260 265 270

Glu Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe
275 280 285

Leu Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala
290 295 300

Thr Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr

305	310	315	320
Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val			
	325	330	335
Lys Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile			
	340	345	350
Val Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr			
	355	360	365
Ala Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala			
	370	375	380
Gln Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met			
385	390	395	400
Ser Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu			
	405	410	415
Leu Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val			
	420	425	430
Ser Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala			
	435	440	445
Pro Glu Lys Gln Met Ala Pro			
450	455		

<210> 36

<211> 1903

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (116)..(1480)

<400> 36

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tgctgtggcc tcggggagtg ggaagtggag gcaggagcct tccttacact tcgcc atg 118

Met

1

agt ttc ctc atc gac tcc agc atc atg att acc tcc cag ata cta ttt 166

Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu Phe

5

10

15

ttt gga ttt ggg tgg ctt ttc ttc atg cgc caa ttg ttt aaa gac tat 214

Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp Tyr

20

25

30

gag ata cgt cag tat gtt gta cag gtg atc ttc tcc gtg acg ttt gca 262

Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe Ala

35

40

45

ttt tct tgc acc atg ttt gag ctc atc atc ttt gaa atc tta gga gta 310
Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly Val
50 55 60 65

ttg aat agc agc tcc cgt tat ttt cac tgg aaa atg aac ctg tgt gta 358
Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys Val
70 75 80

att ctg ctg atc ctg gtt ttc atg gtg cct ttt tac att ggc tat ttt 406
Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr Phe
85 90 95

att gtg agc aat atc cga cta ctg cat aaa caa cga ctg ctt ttt tcc 454
Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe Ser
100 105 110

tgt ctc tta tgg ctg acc ttt atg tat ttc ttc tgg aaa cta gga gat 502
Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly Asp
115 120 125

ccc ttt ccc att ctc agc cca aaa cat ggg atc tta tcc ata gaa cag 550
Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu Gln
130 135 140 145

ctc atc agc cgg gtt ggt gtg att gga gtg act ctc atg gct ctt ctt 598
Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu
150 155 160

tct gga ttt ggt gct gtc aac tgc cca tac act tac atg tct tac ttc 646

Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe	
165	170
175	
ctc agg aat gtg act gac acg gat att cta gcc ctg gaa cgg cga ctg	694
Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu	
180	185
190	
ctg caa acc atg gat atg atc ata agc aaa aag aaa agg atg gca atg	742
Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met	
195	200
205	
gca cgg aga aca atg ttc cag aag ggg gaa gtg cat aac aaa cca tca	790
Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser	
210	215
220	225
ggt ttc tgg gga atg ata aaa agt gtt acc act tca gca tca gga agt	838
Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly Ser	
230	235
240	
gaa aat ctt act ctt att caa cag gaa gtg gat gct ttg gaa gaa tta	886
Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu Leu	
245	250
255	
agc agg cag ctt ttt ctg gaa aca gct gat cta tat gct acc aag gag	934
Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys Glu	
260	265
270	
aga ata gaa tac tcc aaa acc ttc aag ggg aaa tat ttt aat ttt ctt	982
Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe Leu	

275	280	285	
ggg tac ttt ttc tct att tac tgt gtt tgg aaa att ttc atg gct acc			1030
Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala Thr			
290	295	300	305
atc aat att gtt ttt gat cga gtt ggg aaa acg gat cct gtc aca aga			1078
Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr Arg			
	310	315	320
ggc att gag atc act gtg aat tat ctg gga atc caa ttt gat gtg aag			1126
Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val Lys			
	325	330	335
ttt tgg tcc caa cac att tcc ttc att ctt gtt gga ata atc atc gtc			1174
Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile Val			
	340	345	350
aca tcc atc aga gga ttg ctg atc act ctt acc aag ttc ttt tat gcc			1222
Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr Ala			
	355	360	365
atc tct agc agt aag tcc tcc aat gtc att gtc ctg cta tta gca cag			1270
Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala Gln			
370	375	380	385
ata atg ggc atg tac ttt gtc tcc tct gtg ctg ctg atc cga atg agt			1318
Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met Ser			

390

395

400

atg cct tta gaa tac cgc acc ata atc act gaa gtc ctt gga gaa ctg 1366

Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu

405

410

415

cag ttc aac ttc tat cac cgt tgg ttt gat gtg atc ttc ctg gtc agc 1414

Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser

420

425

430

gct ctc tct agc ata ctc ttc ctc tat ttg gct cac aaa cag gca cca 1462

Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro

435

440

445

gag aag caa atg gca cct tgaacttaag cctactacag actgttagag 1510

Glu Lys Gln Met Ala Pro

450

455

gccagtgggtt tcaaaattta gatataagag gggggaaaaa tggaaccagg gcctgacatt 1570

ttataaacia acaaaatgct atggtagcat ttttcacctt catagcatac tccttccccg 1630

tcaggtgata ctatgacat gagtagcatc agccagaaca tgagaggag aactaactca 1690

agacaatact cagcagagag catcccgtgt ggatatgagg ctggtgtaga ggcggagagg 1750

agccaagaaa ctaaaggta aaaatacact ggaactctgg ggcaagacat gtctatggta 1810

gctgagccaa acacgtagga tttccgtttt aaggttcaca tggaaaagggt tatagctttg 1870

ccttgagatt gactcattaa aatcagagac tgt

1903

<210> 37

<211> 322

<212> PRT

<213> Homo sapiens

<400> 37

Met Ser Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser

1

5

10

15

Ser Ser Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala

20

25

30

Gly Ala Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser

35

40

45

Val Ala Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile

50

55

60

Ile Ser Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser

65

70

75

80

His Tyr Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met

85

90

95

Met Gly Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ala

100	105	110
Ser Leu Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp		
115	120	125
Lys Ser Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu		
130	135	140
Leu Ser Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu		
145	150	155
Thr Leu Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val		
165	170	175
Gln Glu His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp		
180	185	190
Met Glu Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe		
195	200	205
Pro Tyr Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr		
210	215	220
Pro Ala Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu		
225	230	235
Ala Glu Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly		
245	250	255

Lys Lys Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg
260 265 270

Ile Asn Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His
275 280 285

Gln Ile Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser
290 295 300

Ala Ala Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp
305 310 315 320

Phe Gln

<210> 38

<211> 1448

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (292).. (1257)

<400> 38

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ccctgccccg cccctcccc tcggcctcgc ggcgacggcg gcggtggcgg cttggacgac 120

tcggagagcc gagtgaagac atttccacct ggacacctga ccatgtgcct gccctgagca 180

gcgaggccca ccaggcatct ctgttgtggg cagcagggcc aggtcctggt ctgtggaccc 240

tcggcagttg gcaggctccc tctgcagtgg ggtctgggcc tcggccccac c atg tcg 297

Met Ser

1

agc ctc ggc ggt ggc tcc cag gat gcc ggc ggc agt agc agc agc agc 345

Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser Ser Ser

5

10

15

acc aat ggc agc ggt ggc agt ggc agc agt ggc cca aag gca gga gca 393

Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala Gly Ala

20

25

30

gca gac aag agt gca gtg gtg gct gcc gcc gca cca gcc tca gtg gca 441

Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser Val Ala

35

40

45

50

gat gac aca cca ccc ccc gag cgt cgg aac aag agc ggt atc atc agt 489

Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile Ile Ser

55

60

65

gag ccc ctc aac aag agc ctg cgc cgc tcc cgc ccg ctc tcc cac tac 537

Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser His Tyr

70

75

80

tct tct ttt ggc agc agt ggt ggt agt ggc ggt ggc agc atg atg ggc 585
 Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met Met Gly

85

90

95

gga gag tct gct gac aag gcc act gcg gct gca gcc gct gcc tcc ctg 633
 Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ala Ser Leu

100

105

110

ttg gcc aat ggg cat gac ctg gcg gcg gcc atg gcg gtg gac aaa agc 681
 Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp Lys Ser

115

120

125

130

aac cct acc tca aag cac aaa agt ggt gct gtg gcc agc ctg ctg agc 729
 Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu Leu Ser

135

140

145

aag gca gag cgg gcc acg gag ctg gca gcc gag gga cag ctg acg ctg 777
 Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu Thr Leu

150

155

160

cag cag ttt gcg cag tcc aca gag atg ctg aag cgc gtg gtg cag gag 825
 Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val Gln Glu

165

170

175

cat ctc ccg ctg atg agc gag gcg ggt gct ggc ctg cct gac atg gag 873
 His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp Met Glu

180

185

190

gct gtg gca ggt gcc gaa gcc ctc aat ggc cag tcc gac ttc ccc tac 921

Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe Pro Tyr
 195 200 205 210

ctg ggc gct ttc ccc atc aac cca ggc ctc ttc att atg acc ccg gca 969
 Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr Pro Ala
 215 220 225

ggt gtg ttc ctg gcc gag agc gcg ctg cac atg gcg ggc ctg gct gag 1017
 Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu Ala Glu
 230 235 240

tac ccc atg cag gga gag ctg gcc tct gcc atc agc tcc ggc aag aag 1065
 Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly Lys Lys
 245 250 255

aag cgg aaa cgc tgc ggc atg tgc gcg ccc tgc cgg cgg cgc atc aac 1113
 Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg Ile Asn
 260 265 270

tgc gag cag tgc agc agt tgt agg aat cga aag act ggc cat cag att 1161
 Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His Gln Ile
 275 280 285 290

tgc aaa ttc aga aaa tgt gag gaa ctc aaa aag aag cct tcc gct gct 1209
 Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser Ala Ala
 295 300 305

ctg gag aag gtg atg ctt ccg acg gga gcc gcc ttc cgg tgg ttt cag 1257
 Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp Phe Gln

310

315

320

tgacggcggc ggaacccaaa gctgccctct ccgtgcaatg tcaactgctcg tgtggtctcc 1317

agcaagggat tcgggcgaag acaaacggat gcacccgtct ttagaaccaa aaatattctc 1377

tcacagattt cattcctggt tttatatata tattttttgt tgtcgtttta acatctccac 1437

gtccctagca t 1448

<210> 39

<211> 313

<212> PRT

<213> Homo sapiens

<400> 39

Met Ala Gly Gln Pro Gly His Met Pro His Gly Gly Ser Ser Asn Asn

1 5 10 15

Leu Cys His Thr Leu Gly Pro Val His Pro Pro Asp Pro Gln Arg His

20 25 30

Pro Asn Thr Leu Ser Phe Arg Cys Ser Leu Ala Asp Phe Gln Ile Glu

35 40 45

Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr Lys Ala Thr Cys

50 55 60

Leu Leu Asp Arg Lys Thr Val Ala Leu Lys Lys Val Gln Ile Phe Glu
65 70 75 80

Met Met Asp Ala Lys Ala Arg Gln Asp Cys Val Lys Glu Ile Gly Leu
85 90 95

Leu Lys Gln Leu Asn His Pro Asn Ile Ile Lys Tyr Leu Asp Ser Phe
100 105 110

Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu Leu Ala Asp Ala Gly
115 120 125

Asp Leu Ser Gln Met Ile Lys Tyr Phe Lys Lys Gln Lys Arg Leu Ile
130 135 140

Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln Leu Cys Ser Ala Val
145 150 155 160

Glu His Met His Ser Arg Arg Val Met His Arg Asp Ile Lys Pro Ala
165 170 175

Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys Leu Gly Asp Leu Gly
180 185 190

Leu Gly Arg Phe Phe Ser Ser Glu Thr Thr Ala Ala His Ser Leu Val
195 200 205

Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His Glu Asn Gly Tyr
210 215 220

Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu Leu Tyr Glu Met
225 230 235 240

Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met Asn Leu Phe Ser
245 250 255

Leu Cys Gln Lys Ile Glu Gln Cys Asp Tyr Pro Pro Leu Pro Gly Glu
260 265 270

His Tyr Ser Glu Lys Leu Arg Glu Leu Val Ser Met Cys Ile Cys Pro
275 280 285

Asp Pro His Gln Arg Pro Asp Ile Gly Tyr Val His Gln Val Ala Lys
290 295 300

Gln Met His Ile Trp Met Ser Ser Thr
305 310

<210> 40

<211> 1597

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (153).. (1091)

<400> 40

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ctccagccgc ccgcgggcca ggcaccgggt cccccagcgg cagccgagcc cgcccgcgcg 120

ccgttcgtgc cctcgtgagg ctggcatgca gg atg gca gga cag ccc ggc cac 173

Met Ala Gly Gln Pro Gly His

1

5

atg ccc cat gga ggg agt tcc aac aac ctc tgc cac acc ctg ggg cct 221

Met Pro His Gly Gly Ser Ser Asn Asn Leu Cys His Thr Leu Gly Pro

10

15

20

gtg cat cct cct gac cca cag agg cat ccc aac acg ctg tct ttt cgc 269

Val His Pro Pro Asp Pro Gln Arg His Pro Asn Thr Leu Ser Phe Arg

25

30

35

tgc tcg ctg gcg gac ttc cag atc gaa aag aag ata ggc cga gga cag 317

Cys Ser Leu Ala Asp Phe Gln Ile Glu Lys Lys Ile Gly Arg Gly Gln

40

45

50

55

ttc agc gag gtg tac aag gcc acc tgc ctg ctg gac agg aag aca gtg 365

Phe Ser Glu Val Tyr Lys Ala Thr Cys Leu Leu Asp Arg Lys Thr Val

60

65

70

gct ctg aag aag gtg cag atc ttt gag atg atg gac gcc aag gcg agg 413

Ala Leu Lys Lys Val Gln Ile Phe Glu Met Met Asp Ala Lys Ala Arg

75

80

85

cag gac tgt gtc aag gag atc ggc ctc ttg aag caa ctg aac cac cca 461
 Gln Asp Cys Val Lys Glu Ile Gly Leu Leu Lys Gln Leu Asn His Pro
 90 95 100

aat atc atc aag tat ttg gac tcg ttt atc gaa gac aac gag ctg aac 509
 Asn Ile Ile Lys Tyr Leu Asp Ser Phe Ile Glu Asp Asn Glu Leu Asn
 105 110 115

att gtg ctg gag ttg gct gac gca ggg gac ctc tcg cag atg atc aag 557
 Ile Val Leu Glu Leu Ala Asp Ala Gly Asp Leu Ser Gln Met Ile Lys
 120 125 130 135

tac ttt aag aag cag aag cgg ctc atc ccg gag agg aca gta tgg aag 605
 Tyr Phe Lys Lys Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys
 140 145 150

tac ttt gtg cag ctg tgc agc gcc gtg gag cac atg cat tca cgc cgg 653
 Tyr Phe Val Gln Leu Cys Ser Ala Val Glu His Met His Ser Arg Arg
 155 160 165

gtg atg cac cga gac atc aag cct gcc aac gtg ttc atc aca gcc acg 701
 Val Met His Arg Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr
 170 175 180

ggc gtc gtg aag ctc ggt gac ctt ggt ctg ggc cgc ttc ttc agc tct 749
 Gly Val Val Lys Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser
 185 190 195

gag acc acc gca gcc cac tcc cta gtg ggg acg ccc tac tac atg tca 797

Glu Thr Thr Ala Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser	
200	215
ccg gag agg atc cat gag aac ggc tac aac ttc aag tcc gac atc tgg	845
Pro Glu Arg Ile His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp	
220	230
tcc ttg ggc tgt ctg ctg tac gag atg gca gcc ctc cag agc ccc ttc	893
Ser Leu Gly Cys Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe	
235	245
tat gga gat aag atg aat ctc ttc tcc ctg tgc cag aag atc gag cag	941
Tyr Gly Asp Lys Met Asn Leu Phe Ser Leu Cys Gln Lys Ile Glu Gln	
250	260
tgt gac tac ccc cca ctc ccc ggg gag cac tac tcc gag aag tta cga	989
Cys Asp Tyr Pro Pro Leu Pro Gly Glu His Tyr Ser Glu Lys Leu Arg	
265	275
gaa ctg gtc agc atg tgc atc tgc cct gac ccc cac cag aga cct gac	1037
Glu Leu Val Ser Met Cys Ile Cys Pro Asp Pro His Gln Arg Pro Asp	
280	295
atc gga tac gtg cac cag gtg gcc aag cag atg cac atc tgg atg tcc	1085
Ile Gly Tyr Val His Gln Val Ala Lys Gln Met His Ile Trp Met Ser	
300	310
agc acc tgagcgtgga tgcaccgtgc cttatcaaag ccagcaccac tttgccttac	1141
Ser Thr	

ttgagtcgtc ttctcttcga gtggccacct ggtagcctag aacagctaag accacagggt 1201
 tcagcaggtt ccccaaaagg ctgcccagcc ttacagcaga tgctgaaggc agagcagctg 1261
 agggaggggc gctggccaca tgctactgat ggtagattc caaagtcctt tctttatact 1321
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 cctgtatctg gattgtaatg tgaatcttta gggtaattcc tccagtgacc tgtcaaggct 1441
 tatgctaaca ggagacttgc aggagaccgt gtgatttgtg tagtgagcct ttgaaaatgg 1501
 ttagtaccgg gttcagttta gttcttggtg tcttttcaat caagctgtgt gcttaattta 1561
 ctctgttgta aagggataaa gtggaaatca tttttt 1597

<210> 41

<211> 371

<212> PRT

<213> Homo sapiens

<400> 41

Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn Tyr Pro Pro

1 5 10 15

Pro Asn Pro Gly Tyr Pro Gly Gly Pro Gln Pro Pro Met Pro Pro Tyr

20 25 30

Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro Pro Phe Gln

35

40

45

Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro Ser Pro Tyr

50

55

60

Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro

65

70

75

80

Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro Tyr Pro Gln

85

90

95

Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe Pro Pro Asn

100

105

110

Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro Asp Ser Pro

115

120

125

Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr Tyr Asp Asn

130

135

140

Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile Arg Gln Ala

145

150

155

160

Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu Ser Val Thr

165

170

175

Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val Lys Gly Phe

180	185	190
Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala Val Phe Phe		
195	200	205
Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg Arg Lys His		
210	215	220
Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser Leu Ser Tyr		
225	230	235 240
Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala Val Ile Met		
245	250	255
Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val Ile Phe Ser		
260	265	270
Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val Leu Leu Val		
275	280	285
Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile Phe Ile Arg		
290	295	300
Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala Leu Leu Phe		
305	310	315 320
Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Leu Gly Asn Lys Gln		
325	330	335

Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu Asn Leu Tyr
340 345 350

Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile Leu Thr Ile Ile Gly Arg
355 360 365

Ala Lys Glu
370

<210> 42

<211> 1781

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91)..(1203)

<400> 42

attggccatc accgcgcggc cgcgcagcgg acaccgtgcg taccggcctg cggcgcccgg 60

ccaccggggc ggaccgcgga acccgaggcc atg tcc cat gaa aag agt ttt ttg 114

Met Ser His Glu Lys Ser Phe Leu

1

5

gtg tct ggg gac aac tat cct ccc ccc aac cct gga tat ccg ggg ggg 162

Val Ser Gly Asp Asn Tyr Pro Pro Pro Asn Pro Gly Tyr Pro Gly Gly

10

15

20

ccc cag cca ccc atg ccc ccc tat gct cag cct ccc tac cct ggg gcc	210
Pro Gln Pro Pro Met Pro Pro Tyr Ala Gln Pro Pro Tyr Pro Gly Ala	
25 30 35 40	
cct tac cca cag ccc cct ttc cag ccc tcc ccc tac ggt cag cca ggg	258
Pro Tyr Pro Gln Pro Pro Phe Gln Pro Ser Pro Tyr Gly Gln Pro Gly	
45 50 55	
tac ccc cat ggc ccc agc ccc tac ccc caa ggg ggc tac cca cag ggt	306
Tyr Pro His Gly Pro Ser Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly	
60 65 70	
ccc tac ccc caa ggg ggc tac cca cag ggc ccc tac cca caa gag ggc	354
Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Glu Gly	
75 80 85	
tac cca cag ggc ccc tac ccc caa ggg ggc tac ccc cag ggg cca tat	402
Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr	
90 95 100	
ccc cag agc ccc ttc ccc ccc aac ccc tat gga cag cca cag gtc ttc	450
Pro Gln Ser Pro Phe Pro Pro Asn Pro Tyr Gly Gln Pro Gln Val Phe	
105 110 115 120	
cca gga caa gac cct gac tca ccc cag cat gga aac tac cag gag gag	498
Pro Gly Gln Asp Pro Asp Ser Pro Gln His Gly Asn Tyr Gln Glu Glu	
125 130 135	

ggt ccc cca tcc tac tat gac aac cag gac ttc cct gcc acc aac tgg 546
 Gly Pro Pro Ser Tyr Tyr Asp Asn Gln Asp Phe Pro Ala Thr Asn Trp

140

145

150

gat gac aag agc atc cga cag gcc ttc atc cgc aag gtg ttc cta gtg 594
 Asp Asp Lys Ser Ile Arg Gln Ala Phe Ile Arg Lys Val Phe Leu Val

155

160

165

ctg acc ttg cag ctg tcg gtg acc ctg tcc acg gtg tct gtg ttc act 642
 Leu Thr Leu Gln Leu Ser Val Thr Leu Ser Thr Val Ser Val Phe Thr

170

175

180

ttt gtt gcg gag gtg aag ggc ttt gtc cgg gag aat gtc tgg acc tac 690
 Phe Val Ala Glu Val Lys Gly Phe Val Arg Glu Asn Val Trp Thr Tyr

185

190

195

200

tat gtc tcc tat gct gtc ttc ttc atc tct ctc atc gtc ctc agc tgt 738
 Tyr Val Ser Tyr Ala Val Phe Phe Ile Ser Leu Ile Val Leu Ser Cys

205

210

215

tgt ggg gac ttc cgg cga aag cac ccc tgg aac ctt gtt gca ctg tcg 786
 Cys Gly Asp Phe Arg Arg Lys His Pro Trp Asn Leu Val Ala Leu Ser

220

225

230

gtc ctg acc gcc agc ctg tcg tac atg gtg ggg atg atc gcc agc ttc 834
 Val Leu Thr Ala Ser Leu Ser Tyr Met Val Gly Met Ile Ala Ser Phe

235

240

245

tac aac acc gag gca gtc atc atg gcc gtg ggc atc acc aca gcc gtc 882

Tyr Asn Thr Glu Ala Val Ile Met Ala Val Gly Ile Thr Thr Ala Val
250 255 260

tgc ttc acc gtc gtc atc ttc tcc atg cag acc cgc tac gac ttc acc 930
Cys Phe Thr Val Val Ile Phe Ser Met Gln Thr Arg Tyr Asp Phe Thr
265 270 275 280

tca tgc atg ggc gtg ctc ctg gtg agc atg gtg gtg ctc ttc atc ttc 978
Ser Cys Met Gly Val Leu Leu Val Ser Met Val Val Leu Phe Ile Phe
285 290 295

gcc att ctc tgc atc ttc atc cgg aac cgc atc ctg gag atc gtg tac 1026
Ala Ile Leu Cys Ile Phe Ile Arg Asn Arg Ile Leu Glu Ile Val Tyr
300 305 310

gcc tca ctg ggc gct ctg ctc ttc acc tgc ttc ctc gca gtg gac acc 1074
Ala Ser Leu Gly Ala Leu Leu Phe Thr Cys Phe Leu Ala Val Asp Thr
315 320 325

cag ctg ctg ctg ggg aac aag cag ctg tcc ctg agc cca gaa gag tat 1122
Gln Leu Leu Leu Gly Asn Lys Gln Leu Ser Leu Ser Pro Glu Glu Tyr
330 335 340

gtg ttt gct gcg ctg aac ctg tac aca gac atc atc aac atc ttc ctg 1170
Val Phe Ala Ala Leu Asn Leu Tyr Thr Asp Ile Ile Asn Ile Phe Leu
345 350 355 360

tac atc ctc acc atc att ggc cgc gcc aag gag tagccgagct ccagctcgcct 1223
Tyr Ile Leu Thr Ile Ile Gly Arg Ala Lys Glu

365

370

gtgcccgc aggtggcacg gctggcctgg accctgcccc tggcacggca gtgccagctg 1283

tacttcccct ctctcttgtc ccagggcaca gcctagggaa aaggatgcct ctctccaacc 1343

ctcctgtatg tacactgcag atacttccat ttggacccgc tgtggccaca gcatggcccc 1403

tttagtcctc ccgccccgc caaggggcag caaggccacg tttccgtgcc acctcctgtc 1463

tactcattgt tgcatgagcc ctgtctgcca gccacccca gggactgggg gcagcaccag 1523

gtcccgggga gagggattga gccaagaggt gaggggtgcac gtcttcctc ctgtcccagc 1583

tccccagcct ggcgtagagc accctcccc tccccccac cccctggag tgctgccctc 1643

tggggacatg cggagtgggg gtcttatccc tgtgctgagc cctgagggca gagaggatgg 1703

catgtttcag gggaggggga agccttcctc tcaatttggt gtcagtgaat ttccaataaa 1763

tgggatttgc tctctgcc 1781

<210> 43

<211> 393

<212> PRT

<213> Homo sapiens

<400> 43

Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala
1 5 10 15

Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro
20 25 30

Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu
35 40 45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu
50 55 60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr
65 70 75 80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg
85 90 95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met
100 105 110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg
115 120 125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln
130 135 140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala
145 150 155 160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala
165 170 175

Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val
180 185 190

Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu
195 200 205

Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser
210 215 220

Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr
225 230 235 240

His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly
245 250 255

Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly
260 265 270

Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala
275 280 285

Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr
290 295 300

Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn

305 310 315 320

Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu

325 330 335

Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly

340 345 350

His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala

355 360 365

Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu

370 375 380

Leu Val Pro Gly Pro Glu Lys Glu Asn

385 390

<210> 44

<211> 2396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)..(1228)

<400> 44

agctgtgcac tctccatcca gctgtgcgct ctcgtcgga gtcccagcc atg tcc gac 58

Met Ser Asp

1

gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg 106

Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro

5

10

15

cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc 154

Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser

20

25

30

35

gaa ggg gcc gcc gcc gcc gcc gcc tcg ccg cca ctg ctg cgc tgc cta 202

Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu

40

45

50

gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg 250

Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg

55

60

65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg 298

Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu

70

75

80

cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg 346

Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu

85

90

95

tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg 394

Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala

100	105	110	115	
ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga				442
Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly				
	120	125	130	
gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg				490
Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val				
	135	140	145	
act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt				538
Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe				
	150	155	160	
gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc				586
Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val				
	165	170	175	
ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac				634
Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His				
180	185	190	195	
atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca				682
Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr				
	200	205	210	
gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag				730
Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu				
	215	220	225	

gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act	778
Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr	
230 235 240	
gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att	826
Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile	
245 250 255	
gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc	874
Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu	
260 265 270 275	
ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg	922
Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu	
280 285 290	
acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat	970
Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn	
295 300 305	
cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg	1018
Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val	
310 315 320	
tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt	1066
Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser	
325 330 335	

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag 1114
 Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys
 340 345 350 355

ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg 1162
 Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met
 360 365 370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca 1210
 Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro
 375 380 385

ggg cca gag aag gag aac tagggcaagt ggctgtgaga ccctagagac 1258
 Gly Pro Glu Lys Glu Asn
 390

cagcgaaggg agaagttggg aagctacgtt ctgttggcca ccagacttgc atttcagcct 1318

ctgtcataat gctctgcctt ccttcccccg aagttctctg tggatgatgac cgctctcccc 1378

tgccccctccc cgcttctga cctctgaaga ggttgggaag tgaccatttg gatgtctggg 1438

ccctgccaaag gcgacaggga gggtcagagg gaggccggct gcttctgcc cccacccttt 1498

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tgtgctttca cctctgctc atctttctc cgtccctgc cccgccacct ccccaaagaa 1618

ttgaaacgtc agctcaggat atggggccaa tctctgtgag tccagcatgt acctgtctct 1678

ccctagtgtc ccttcagcct gggctgacca gtgcccgcct ctgggcttga ccagttccca 1738
 atctcgctct ctgtcccca cttcttaagc acaattgggc ttcttccatc tccaggtttt 1798
 ctgccattct taaccaaggc agccccaagc ctcttgggga ggcagggcaa aaacaggtgc 1858
 cctcatcgtg gtctgtgcca tgtcccgtct ctatggtggt tgaggagaaa ggcggggaag 1918
 cttectcage cttgcagata tgtgtggcat ttactagcca gagctctgaa aggcagtgc 1978
 gtctgtttct tgtactggga ccaaagtaaa aatccaagca cattcccctt gcagttaggg 2038
 gaggccctac tgccttctca aagcagagag gcagcttctc aaactcagcc caaaactctg 2098
 ttacatggg tggggagatg gagcaggga gtacagagtg gcatggtcag gacctgggcc 2158
 attgcaacca aaatggggac ttcttgggta gggaggtcac tccctctact cactgagcta 2218
 ggattaggga gggttattgc cccaaccatt gcaatgggag gtggaggga aggctcagcc 2278
 tctcattgt ctaaagagg cctaaatgtg tgaagtgcga tttctgcttt tgtgtacccc 2338
 accaccccat taccacagct gcctttgtgt gtttgtgtca ataaaaagcc aaaccctg 2396

<210> 45

<211> 393

<212> PRT

<213> Homo sapiens

<400> 45

Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala

1 5 10 15

Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro

20 25 30

Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu

35 40 45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu

50 55 60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr

65 70 75 80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg

85 90 95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met

100 105 110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg

115 120 125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln

130 135 140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala
145 150 155 160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala
165 170 175

Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val
180 185 190

Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu
195 200 205

Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser
210 215 220

Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr
225 230 235 240

His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly
245 250 255

Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly
260 265 270

Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala
275 280 285

Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr

290	295	300
Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn		
305	310	315 320
Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu		
325	330	335
Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly		
340	345	350
His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala		
355	360	365
Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu		
370	375	380
Leu Val Pro Gly Pro Glu Lys Gln Asn		
385	390	

<210> 46

<211> 2396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)..(1228)

<400> 46

agctgtgcac tctccatcca gctgtgcgct ctcgtcggga gtcccagcc atg tcc gac 58

Met Ser Asp

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gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg 106

Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro

5

10

15

cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc 154

Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser

20

25

30

35

gaa ggg gcc gcc gcc gcc gcc gcc tgc ccg cca ctg ctg cgc tgc cta 202

Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu

40

45

50

gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg 250

Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg

55

60

65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg 298

Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu

70

75

80

cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg 346

Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu

85

90

95

tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg 394
Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala
100 105 110 115

ggc gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga 442
Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly
120 125 130

gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg 490
Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val
135 140 145

act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt 538
Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe
150 155 160

gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc 586
Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val
165 170 175

ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac 634
Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His
180 185 190 195

atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca 682
Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr
200 205 210

gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag 730
Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu
215 220 225

gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act 778
Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr
230 235 240

gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att 826
Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile
245 250 255

gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc 874
Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu
260 265 270 275

ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg 922
Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu
280 285 290

acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat 970
Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn
295 300 305

cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg 1018
Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val
310 315 320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt 1066

Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser

325

330

335

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag 1114

Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys

340

345

350

355

ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg 1162

Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met

360

365

370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca 1210

Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro

375

380

385

ggg cca gag aag cag aac tagggcaagt ggctgtgaga ccctagagac 1258

Gly Pro Glu Lys Gln Asn

390

cagcgaaggg agaagttggg aagctacgtt ctgttgcca ccagacttgc atttcagcct 1318

ctgtcataat gctctgccct cctcccccg aagttctctg tggtgatgac cgctctcccc 1378

tgccccctccc cgcttcctga cctctgaaga gggtgggaag tgaccatttg gatgtctggg 1438

ccctgccaaag ggcacaggga gggtcagagg gaggccggct gcttcctgcc cccacccttt 1498

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<210> 47

<211> 138

<212> PRT

<213> Homo sapiens

<400> 47

Met Ile Ser Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly

1 5 10 15

Phe Gly Val Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys

20 25 30

Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe

35 40 45

Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys

50 55 60

Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile

65 70 75 80

Gly Trp Pro Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu

85 90 95

Leu Phe Arg Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val

100 105 110

Pro Val Leu Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val

136/754

115

120

125

Asp Lys Val Gly Glu Ser Asn Asn Met Val

130

135

<210> 48

<211> 2976

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (110)..(523)

<400> 48

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accctgggct ttccgaggtg ctgtcgcgc tgtccccacc actgcagcc atg atc tcc 118

Met Ile Ser

1

tta acg gac acg cag aaa att gga atg gga tta aca gga ttt gga gtg 166

Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly Phe Gly Val

5

10

15

ttt ttc ctg ttc ttt gga atg att ctc ttt ttt gac aaa gca cta ctg 214

Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys Ala Leu Leu

20

25

30

35

gct att gga aat gtt tta ttt gta gcc ggc ttg gct ttt gta att ggt 262

Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe Val Ile Gly

40

45

50

tta gaa aga aca ttc aga ttc ttc ttc caa aaa cat aaa atg aaa gct 310

Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys Met Lys Ala

55

60

65

aca ggt ttt ttt ctg ggt ggt gta ttt gta gtc ctt att ggt tgg cct 358

Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile Gly Trp Pro

70

75

80

ttg ata ggc atg atc ttc gaa att tat gga ttt ttt ctc ttg ttc agg 406

Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu Leu Phe Arg

85

90

95

ggc ttc ttt cct gtc gtt gtt ggc ttt att aga aga gtg cca gtc ctt 454

Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val Pro Val Leu

100

105

110

115

gga tcc ctc cta aat tta cct gga att aga tca ttt gta gat aaa gtt 502

Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val

120

125

130

gga gaa agc aac aat atg gta taacaacaag tgaatttgaa gactcattta 553

Gly Glu Ser Asn Asn Met Val

135

aaatattgtg ttatttataa agtcatttga agaattattca gcacaaaatt aaattacatg 613

aaatagcttg taatgttctt tacaggagtt taaaacgtat agcctacaaa gtaccagcag 673

caaattagca aagaagcagt gaaaacaggc ttctactcaa gtgaactaag aagaagtcag 733

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attctttact aacttttagt tactaaatta tagctaagtt ttgtcagcag catactcgg 1213

aaagtctcat acttcttggg agtctgccct cctaagtatc tgtctatatc attcattacg 1273

tgtaagtatt taacaaaaaa gcattcttga ccatgaatga agtagtttgt ttcatagctt 1333

gtctcattga atagtattat tgaagatact aaatgatgca aaccaaattg attttttcca 1393

tgcatgatg taatttttct ttcttcttct ttttttttaa attttagcag tggcttatta 1453

tttgtttttc ataaattaa ataacttttg ataatgttta ctttaagaca tgtaacatgt 1513

taaaaggtta aacttatggc tgttttttaa gggctattca tttaatctga gttttccctt 1573

attttcagct ttttcctagc atataatagt cattaagcat gacatatacct tcatatgac 1633

actcatcttg agttaattag aaaataacctg agttcacgtg ctaaagtcac ttcactgtaa 1693

taaactgact atggtttctt aagaacatga cactaaaaaa aaagtgggtt ttttccaccg 1753

ttgctgatta ttagacagta ggaaatagct gttttcttta gttttacaag atgtgacagc 1813

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ttgcactggt ttgttttttt aacagttgca aagcttttta atgcataaaa gtataattga 1933

aatctgtggt atttatttac aaacatgtct acaaaaatag attacagctt attttatttt 1993

tagttaaatc tcttaataca cagagaactc ccaatcttgc tcatctaaat aaggaaagac 2053

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gttaatggaa taataagagg ctactgttgt gtctaagtgt cttcaaaaaa gtaataaccc 2233

cacttgaga gtgtcaaata catactttga ggattgactt tatataaggt gccctgtaga 2293

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 gaatgttttt cttttccct tataaattgt aattcctgaa atactgctgc tttaaaaagt 2893
 cccactgtca gattatatta tctaacaatt gaatattgta aatatacttg tcttacctct 2953
 caataaaagg gtacttttct att 2976

<210> 49

<211> 359

<212> PRT

<213> Homo sapiens

<400> 49

Met Ser Lys Glu Thr Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe

1 5 10 15

His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln

20 25 30

Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val

35 40 45

Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro

50 55 60

Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met

65 70 75 80

Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile

85 90 95

Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser

100 105 110

Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu

115 120 125

His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp

130 135 140

Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg
145 150 155 160

Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His
165 170 175

Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr
180 185 190

Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu
195 200 205

Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro
210 215 220

Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile
225 230 235 240

Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser
245 250 255

Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser
260 265 270

Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe
275 280 285

Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His
290 295 300

Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met
305 310 315 320

Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser
325 330 335

Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser
340 345 350

Arg Ser Thr Thr His Leu Ile
355

<210> 50

<211> 2636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (327)..(1403)

<400> 50

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atgttaatat attggcaaca attattcagt tattttcaagt accattggaa gaggaaggac 120

aacgtggtgg acctatcctt gcaccagagg agattaagac tattttttggt agcatcccag 180

atatctttga tgtacacact aagataaagg atgatcttga agaccttata gttaattggg 240

atgagagcaa aagcattggg gacatttttc tgaaatattc aaaagatttg gtaaaaacct 300

accctccctt tgtaaacttc tttgaa atg agc aag gaa aca att att aaa tgt 353

Met Ser Lys Glu Thr Ile Ile Lys Cys

1

5

gaa aaa cag aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca 401

Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala

10

15

20

25

aaa cca gaa tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca 449

Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro

30

35

40

gta cag agg tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag 497

Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys

45

50

55

cat aca gct gat gaa aat cca gac aaa agc act tta gaa aaa gct att 545

His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile

60

65

70

gga tca ctg aag gaa gta atg acg cat att aat gag gat aag aga aaa 593

Gly Ser Leu Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys

75

80

85

aca gaa gct caa aag caa att ttt gat gtt gtt tat gaa gta gat gga 641
 Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly
 90 95 100 105

tgc cca gct aat ctt tta tct tct cac cga agc tta gta cag cgg gtt 689
 Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val
 110 115 120

gaa aca att tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta 737
 Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val
 125 130 135

act ctc ttc ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac 785
 Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His
 140 145 150

aag gtt att ggc act ttt agg agt cct cat ggc caa acc cga ccc cca 833
 Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro
 155 160 165

gct tct ctt aag cat att cac cta atg cct ctt tct cag att aag aag 881
 Ala Ser Leu Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys
 170 175 180 185

gta ttg gac ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg 929
 Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu
 190 195 200

ctt gtg agg cca cca aca gag cag gca aat gtg cta ctc agt ttc cag 977
 146/754

Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln

205

210

215

atg aca tca gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt 1025

Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys

220

225

230

cga cat gta gct aac acc att tgt aaa gca gat gct gag aat ctt att 1073

Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile

235

240

245

tat act gct gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac 1121

Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp

250

255

260

265

agt aca ttg agt aga gca tca aga gca ata aaa aag act tca aaa aag 1169

Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys

270

275

280

gtt aca aga gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga 1217

Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg

285

290

295

agg gct ctt atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc 1265

Arg Ala Leu Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser

300

305

310

agc aat gat aag cat gta atg agt cgt ctt tct agc aca tca tca tta 1313

Ser Asn Asp Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu

315

320

325

gca ggt atc cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa 1361

Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu

330

335

340

345

agg aga agt cat acg tta agt aga tct aca act cat ttg ata 1403

Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr His Leu Ile

350

355

tgaagcgta ccaaaatctt aaattataga aatgtataga cacctcatac tcaaataaga 1463

aactgactta aatggtactt gtaattagca cttggtgaaa gctggaagga agataaataa 1523

cactaaacta tgctatttga tttttcttct tgaaagagta aggtttacct gttacatttt 1583

caagttaatt catgtaaaaa atgatagtga ttttgatgta atttatctct tgtttgaatc 1643

tgtcattcaa aggccaataa tttaagttgc tatcagctga tattagtagc tttgcaaccc 1703

tgatagagta aataaatttt atgggcgggt gccaaatact gctgtgaatc tatttgtata 1763

gtatccatga atgaatttat ggaaatagat atttgtgcag ctcaatttat gcagagatta 1823

aatgacatca taatactgga tgaaaacttg catagaattc tgattaaata gtgggtctgt 1883

ttcacatgtg cagtttgaag tatttaaata accactcctt tcacagttta ttttcttctc 1943

aagcgttttc aagatctagc atgtggattt taaaagattt gccctcatta acaagaataa 2003

catttaaagg agattgtttc aaaatatattt tgcaaattga gataaggaca gaaagattga 2063
gaaacattgt atattttgca aaaacaagat gtttgtagct gtttcagaga gaggtaggta 2123
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<210> 51

<211> 883

<212> PRT

<213> Homo sapiens

<400> 51

Met Ala Glu Asn Ser Val Leu Thr Ser Thr Thr Gly Arg Thr Ser Leu
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Ala Asp Ser Ser Ile Phe Asp Ser Lys Val Thr Glu Ile Ser Lys Glu
20 25 30

Asn Leu Leu Ile Gly Ser Thr Ser Tyr Val Glu Glu Glu Met Pro Gln
35 40 45

Ile Glu Thr Arg Val Ile Leu Val Gln Glu Ala Gly Lys Gln Glu Glu
50 55 60

Leu Thr Lys Ala Leu Lys Asp Ile Lys Val Gly Phe Val Lys Met Glu
65 70 75 80

Ser Val Glu Glu Phe Glu Gly Leu Asp Ser Pro Glu Phe Glu Asn Val
85 90 95

Phe Val Val Thr Asp Phe Gln Asp Ser Val Phe Asn Asp Leu Tyr Lys
100 105 110

Ala Asp Cys Arg Val Ile Gly Pro Pro Val Val Leu Asn Cys Ser Gln
115 120 125

Lys Gly Glu Pro Leu Pro Phe Ser Cys Arg Pro Leu Tyr Cys Thr Ser
130 135 140

Met Met Asn Leu Val Leu Cys Phe Thr Gly Phe Arg Lys Lys Glu Glu
150/754

145	150	155	160
Leu Val Arg Leu Val Thr Leu Val His His Met Gly Gly Val Ile Arg			
165	170	175	
Lys Asp Phe Asn Ser Lys Val Thr His Leu Val Ala Asn Cys Thr Gln			
180	185	190	
Gly Glu Lys Phe Arg Val Ala Val Ser Leu Gly Thr Pro Ile Met Lys			
195	200	205	
Pro Glu Trp Ile Tyr Lys Ala Trp Glu Arg Arg Asn Glu Gln Asp Phe			
210	215	220	
Tyr Ala Ala Val Asp Asp Phe Arg Asn Glu Phe Lys Val Pro Pro Phe			
225	230	235	240
Gln Asp Cys Ile Phe Ser Phe Leu Gly Phe Ser Asp Glu Glu Lys Thr			
245	250	255	
Asn Met Glu Glu Met Thr Glu Met Gln Gly Gly Lys Tyr Leu Pro Leu			
260	265	270	
Gly Asp Glu Arg Cys Thr His Leu Val Val Glu Glu Asn Ile Val Lys			
275	280	285	
Asp Leu Pro Phe Glu Pro Ser Lys Lys Leu Tyr Val Val Lys Gln Glu			
290	295	300	

Trp Phe Trp Gly Ser Ile Gln Met Asp Ala Arg Ala Gly Glu Thr Met
305 310 315 320

Tyr Leu Tyr Glu Lys Ala Asn Thr Pro Glu Leu Lys Lys Ser Val Ser
325 330 335

Met Leu Ser Leu Asn Thr Pro Asn Ser Asn Arg Lys Arg Arg Arg Leu
340 345 350

Lys Glu Thr Leu Ala Gln Leu Ser Arg Asp Thr Asp Val Ser Pro Phe
355 360 365

Pro Pro Arg Lys Arg Pro Ser Ala Glu His Ser Leu Ser Ile Gly Ser
370 375 380

Leu Leu Asp Ile Ser Asn Thr Pro Glu Ser Ser Ile Asn Tyr Gly Asp
385 390 395 400

Thr Pro Lys Ser Cys Thr Lys Ser Ser Lys Ser Ser Thr Pro Val Pro
405 410 415

Ser Lys Gln Ser Ala Arg Trp Gln Val Ala Lys Glu Leu Tyr Gln Thr
420 425 430

Glu Ser Asn Tyr Val Asn Ile Leu Ala Thr Ile Ile Gln Leu Phe Gln
435 440 445

Val Pro Leu Glu Glu Glu Gly Gln Arg Gly Gly Pro Ile Leu Ala Pro
450 455 460

Glu Glu Ile Lys Thr Ile Phe Gly Ser Ile Pro Asp Ile Phe Asp Val
465 470 475 480

His Thr Lys Ile Lys Asp Asp Leu Glu Asp Leu Ile Val Asn Trp Asp
485 490 495

Glu Ser Lys Ser Ile Gly Asp Ile Phe Leu Lys Tyr Ser Lys Asp Leu
500 505 510

Val Lys Thr Tyr Pro Pro Phe Val Asn Phe Phe Glu Met Ser Lys Glu
515 520 525

Thr Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu
530 535 540

Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu
545 550 555 560

Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu
565 570 575

Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr
580 585 590

Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met Thr His Ile Asn
595 600 605

Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val

610	615	620	
Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser			
625	630	635	640
Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp			
	645	650	655
Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile			
	660	665	670
Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly			
	675	680	685
Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His Leu Met Pro Leu			
	690	695	700
Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His			
705	710	715	720
Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val			
	725	730	735
Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp			
	740	745	750
Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp			
	755	760	765

Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn
770 775 780

Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys
785 790 795 800

Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro
805 810 815

Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His Gly Ser Val Glu
820 825 830

Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met Ser Arg Leu Ser
835 840 845

Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu
850 855 860

Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr
865 870 875 880

His Leu Ile

<210> 52

<211> 3910

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<213> Homo sapiens

<220>

<221> CDS

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tcc act act ggg agg act agc ttg gca gac tct tcc att ttt gat tct 100

Ser Thr Thr Gly Arg Thr Ser Leu Ala Asp Ser Ser Ile Phe Asp Ser

10

15

20

aaa gtt act gag att tcc aag gaa aac tta ctt att gga tct act tca 148

Lys Val Thr Glu Ile Ser Lys Glu Asn Leu Leu Ile Gly Ser Thr Ser

25

30

35

40

tat gta gaa gaa gag atg cct cag att gaa aca aga gtg ata ttg gtt 196

Tyr Val Glu Glu Glu Met Pro Gln Ile Glu Thr Arg Val Ile Leu Val

45

50

55

caa gaa gct gga aaa caa gaa gaa ctt aca aaa gcc tta aag gac att 244

Gln Glu Ala Gly Lys Gln Glu Glu Leu Thr Lys Ala Leu Lys Asp Ile

60

65

70

aaa gtg ggc ttt gta aag atg gag tca gtg gaa gaa ttt gaa ggt ttg 292

Lys Val Gly Phe Val Lys Met Glu Ser Val Glu Glu Phe Glu Gly Leu

75

80

85

gat tct ccg gaa ttt gaa aat gta ttt gta gtc acg gac ttt cag gat	340
Asp Ser Pro Glu Phe Glu Asn Val Phe Val Val Thr Asp Phe Gln Asp	
90 95 100	
tct gtc ttt aat gac ctc tac aag gct gat tgt aga gtt att gga cca	388
Ser Val Phe Asn Asp Leu Tyr Lys Ala Asp Cys Arg Val Ile Gly Pro	
105 110 115 120	
cca gtt gta tta aat tgt tca caa aaa gga gag cct ttg cca ttt tca	436
Pro Val Val Leu Asn Cys Ser Gln Lys Gly Glu Pro Leu Pro Phe Ser	
125 130 135	
tgt cgc ccg ttg tat tgt aca agt atg atg aat cta gta cta tgc ttt	484
Cys Arg Pro Leu Tyr Cys Thr Ser Met Met Asn Leu Val Leu Cys Phe	
140 145 150	
act gga ttt agg aaa aaa gaa gaa cta gtc agg ttg gtg aca ttg gtc	532
Thr Gly Phe Arg Lys Lys Glu Glu Leu Val Arg Leu Val Thr Leu Val	
155 160 165	
cat cac atg ggt gga gtt att cga aaa gac ttt aat tca aaa gtt aca	580
His His Met Gly Gly Val Ile Arg Lys Asp Phe Asn Ser Lys Val Thr	
170 175 180	
cat ttg gtg gca aat tgt aca caa gga gaa aaa ttc agg gtt gct gtg	628
His Leu Val Ala Asn Cys Thr Gln Gly Glu Lys Phe Arg Val Ala Val	
185 190 195 200	

agt cta ggt act cca att atg aag cca gaa tgg att tat aaa gct tgg 676
 Ser Leu Gly Thr Pro Ile Met Lys Pro Glu Trp Ile Tyr Lys Ala Trp
 205 210 215

gaa agg cgg aat gaa cag gat ttc tat gca gca gtt gat gac ttt aga 724
 Glu Arg Arg Asn Glu Gln Asp Phe Tyr Ala Ala Val Asp Asp Phe Arg
 220 225 230

aat gaa ttt aaa gtt cct cca ttt caa gat tgt att ttt agt ttc ctg 772
 Asn Glu Phe Lys Val Pro Pro Phe Gln Asp Cys Ile Phe Ser Phe Leu
 235 240 245

gga ttt tca gat gaa gag aaa acc aat atg gaa gaa atg act gaa atg 820
 Gly Phe Ser Asp Glu Glu Lys Thr Asn Met Glu Glu Met Thr Glu Met
 250 255 260

caa gga ggt aaa tat tta ccg ctt gga gat gaa aga tgc act cac ctt 868
 Gln Gly Gly Lys Tyr Leu Pro Leu Gly Asp Glu Arg Cys Thr His Leu
 265 270 275 280

gta gtt gaa gag aat ata gta aaa gat ctt ccc ttt gaa cct tca aag 916
 Val Val Glu Glu Asn Ile Val Lys Asp Leu Pro Phe Glu Pro Ser Lys
 285 290 295

aaa ctt tat gtt gtc aag caa gag tgg ttc tgg gga agc att caa atg 964
 Lys Leu Tyr Val Val Lys Gln Glu Trp Phe Trp Gly Ser Ile Gln Met
 300 305 310

gat gcc cga gct gga gaa act atg tat tta tat gaa aag gca aat act 1012

Asp Ala Arg Ala Gly Glu Thr Met Tyr Leu Tyr Glu Lys Ala Asn Thr
315 320 325

cct gag ctc aag aaa tca gtg tca atg ctt tct cta aat acc cct aac 1060
Pro Glu Leu Lys Lys Ser Val Ser Met Leu Ser Leu Asn Thr Pro Asn
330 335 340

agc aat cgc aaa cga cgt cgt tta aaa gaa aca ctt gct cag ctt tca 1108
Ser Asn Arg Lys Arg Arg Arg Leu Lys Glu Thr Leu Ala Gln Leu Ser
345 350 355 360

aga gat aca gac gtg tca cca ttt cca ccc cgt aag cgc cca tca gct 1156
Arg Asp Thr Asp Val Ser Pro Phe Pro Pro Arg Lys Arg Pro Ser Ala
365 370 375

gag cat tcc ctt tcc ata ggg tca ctc cta gat atc tcc aac aca cca 1204
Glu His Ser Leu Ser Ile Gly Ser Leu Leu Asp Ile Ser Asn Thr Pro
380 385 390

gag tct agc att aac tat gga gac acc cca aag tct tgt act aag tct 1252
Glu Ser Ser Ile Asn Tyr Gly Asp Thr Pro Lys Ser Cys Thr Lys Ser
395 400 405

tct aaa agc tcc act cca gtt cct tca aag cag tca gca agg tgg caa 1300
Ser Lys Ser Ser Thr Pro Val Pro Ser Lys Gln Ser Ala Arg Trp Gln
410 415 420

gtt gca aaa gag ctt tat caa act gaa agt aat tat gtt aat ata ttg 1348
Val Ala Lys Glu Leu Tyr Gln Thr Glu Ser Asn Tyr Val Asn Ile Leu

425	430	435	440	
gca aca att att cag tta ttt caa gta cca ttg gaa gag gaa gga caa				1396
Ala Thr Ile Ile Gln Leu Phe Gln Val Pro Leu Glu Glu Glu Gly Gln				
	445	450	455	
cgt ggt gga cct atc ctt gca cca gag gag att aag act att ttt ggt				1444
Arg Gly Gly Pro Ile Leu Ala Pro Glu Glu Ile Lys Thr Ile Phe Gly				
	460	465	470	
agc atc cca gat atc ttt gat gta cac act aag ata aag gat gat ctt				1492
Ser Ile Pro Asp Ile Phe Asp Val His Thr Lys Ile Lys Asp Asp Leu				
	475	480	485	
gaa gac ctt ata gtt aat tgg gat gag agc aaa agc att ggt gac att				1540
Glu Asp Leu Ile Val Asn Trp Asp Glu Ser Lys Ser Ile Gly Asp Ile				
	490	495	500	
ttt ctg aaa tat tca aaa gat ttg gta aaa acc tac cct ccc ttt gta				1588
Phe Leu Lys Tyr Ser Lys Asp Leu Val Lys Thr Tyr Pro Pro Phe Val				
505	510	515	520	
aac ttc ttt gaa atg agc aag gaa aca att att aaa tgt gaa aaa cag				1636
Asn Phe Phe Glu Met Ser Lys Glu Thr Ile Ile Lys Cys Glu Lys Gln				
	525	530	535	
aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca aaa cca gaa				1684
Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu				
	540	545	550	

tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca gta cag agg 1732
 Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg

555

560

565

tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag cat aca gct 1780
 Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala

570

575

580

gat gaa aat cca gac aaa agc act tta gaa aaa gct att gga tca ctg 1828
 Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu
 585 590 595 600

aag gaa gta atg acg cat att aat gag gat aag aga aaa aca gaa gct 1876
 Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala

605

610

615

caa aag caa att ttt gat gtt gtt tat gaa gta gat gga tgc cca gct 1924
 Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala

620

625

630

aat ctt tta tct tct cac cga agc tta gta cag cgg gtt gaa aca att 1972
 Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile

635

640

645

tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta act ctc ttc 2020
 Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe

650

655

660

ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac aag gtt att 2068
 Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile
 665 670 675 680

ggc act ttt agg agt cct cat ggc caa acc cga ccc cca gct tct ctt 2116
 Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu
 685 690 695

aag cat att cac cta atg cct ctt tct cag att aag aag gta ttg gac 2164
 Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp
 700 705 710

ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg ctt gtg agg 2212
 Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg
 715 720 725

cca cca aca gag cag gca aat gtg cta ctc agt ttc cag atg aca tca 2260
 Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser
 730 735 740

gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt cga cat gta 2308
 Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val
 745 750 755 760

gct aac acc att tgt aaa gca gat gct gag aat ctt att tat act gct 2356
 Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala
 765 770 775

gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac agt aca ttg 2404

Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu

780

785

790

agt aga gca tca aga gca ata aaa aag act tca aaa aag gtt aca aga 2452

Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg

795

800

805

gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga agg gct ctt 2500

Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu

810

815

820

atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc agc aat gat 2548

Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp

825

830

835

840

aag cat gta atg agt cgt ctt tct agc aca tca tca tta gca ggt atc 2596

Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile

845

850

855

cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa agg aga agt 2644

Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser

860

865

870

cat acg tta agt aga tct aca act cat ttg ata tgaagcgtta ccaaaatctt 2697

His Thr Leu Ser Arg Ser Thr Thr His Leu Ile

875

880

aaattataga aatgtataga cacctcatatc tcaaataaga aactgactta aatgggtactt 2757

gtaattagca cttggtgaaa gctggaagga agataaataa cactaaacta tgctatttga 2817

tttttcttct tgaagagta aggtttacct gttacatttt caagttaatt catgtaaaaa 2877

atgatagtga tttgatgta atttatctct tgtttgaatc tgtcattcaa aggccaataa 2937

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atgggcgggg gccaaatact gctgtgaatc tatttgtata gtatccatga atgaatttat 3057

ggaaatagat atttgtgcag ctcaatttat gcagagatta aatgacatca taatactgga 3117

tgaaaacttg catagaattc tgattaaata gtgggtctgt ttcacatgtg cagtttgaag 3177

tatttaaata accactcctt tcacagttta ttttcttctc aagcgttttc aagatctagc 3237

atgtggattt taaaagattt gccctcatta acaagaataa catttaaagg agattgtttc 3297

aaaatatttt tgcaaattga gataaggaca gaaagattga gaaacattgt atattttgca 3357

aaaacaagat gttttagct gtttcagaga gagtacgga tatttatggt aattttatcc 3417

actagcaaat cttgatttag tttgatagtg tgtggaattt tattttgaag gataagacca 3477

tgggaaaatt gtggtaaaga ctgtttgtac cttcatgaa ataattctga agttgccatc 3537

agttttacta atcttctgtg aaatgcatag atatgcgcat gttcaacttt ttattgtggt 3597

cttataatta aatgtaaaat tgaaaattca tttgctgttt caaagtgtga tatctttcac 3657

aatagccttt ttatagtcag taattcagaa taatcaagtt catatggata aatgcatttt 3717

tatttcctat ttcttttaggg agtgctacaa atgtttgtca cttaaatttc aagtttctgt 3777

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atacctaataa ccc 3910

<210> 53

<211> 622

<212> PRT

<213> Homo sapiens

<400> 53

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Pro His Pro Pro Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn

20 25 30

Lys Glu Leu Ala Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser

35 40 45

Ser Asn Cys Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg

50 55 60

Cys Lys Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys
65 70 75 80

Glu Asn Val Ser Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp
85 90 95

Leu Val Lys Phe Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly
100 105 110

Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His
115 120 125

Leu Pro Met Val Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu
130 135 140

Ile Asp Gly Glu Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln
145 150 155 160

His Met Pro Ile Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn
165 170 175

Met Thr Asp Val Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys
180 185 190

Val Ile Gly Pro Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser
195 200 205

Leu Asn Val Val Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala
166/754

210	215	220	
Val Ala Ala Gly Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly			
225	230	235	240
Ser Ser Leu Asp Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met			
	245	250	255
Ala Leu Gln Asn Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu			
	260	265	270
Ala Lys Met Arg Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln			
	275	280	285
Lys Cys Glu Leu Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp			
	290	295	300
Ala Ile Gly Tyr Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys			
305	310	315	320
Gly Cys Leu Leu Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg			
	325	330	335
Phe Leu Val Gly Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu			
	340	345	350
Leu Ser Ser Val Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe			
	355	360	365

Pro Asp Leu Ala Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile
370 375 380

Val Ala Phe Leu Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly
385 390 395 400

Phe Thr Lys Ala Ser Glu Glu Glu Lys Lys Val Asn Ile Ile Thr Leu
405 410 415

Ala Glu Thr Gly Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu
420 425 430

Ile Arg Lys Pro Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys
435 440 445

Val Ala Arg Tyr Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly
450 455 460

Phe Gly Asn His His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met
465 470 475 480

Val Cys Gly Trp Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His
485 490 495

Cys Ala Thr Thr Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln
500 505 510

Ile Val Ala Cys Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr
515 520 525

Phe His Phe Ser Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln
530 535 540

Ile Ala Phe Leu Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys
545 550 555 560

Gln Ser Lys His Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr
565 570 575

Asn Leu Gly Phe Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys
580 585 590

Phe Gly Leu Val Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr
595 600 605

Met Val Phe His Pro Ala Arg Glu Lys Val Leu Arg Ser Val
610 615 620

<210> 54

<211> 2426

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (104)..(1969)

<400> 54

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gctacttgcc tagtagcctc agccgctgtg ggctcctggg gag atg gag ggg ccg 115

Met Glu Gly Pro

1

ggg ctg ggc tcg cag tgc agg aat cac agc cat ggc ccc cac cct cca 163

Gly Leu Gly Ser Gln Cys Arg Asn His Ser His Gly Pro His Pro Pro

5

10

15

20

gga ttt ggt cga tat ggc atc tgt gca cat gaa aac aaa gaa ctt gcc 211

Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn Lys Glu Leu Ala

25

30

35

aat gca aga gaa gct ctt cct ctt ata gag gac tct agt aac tgt gac 259

Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser Ser Asn Cys Asp

40

45

50

att gtc aaa gct act caa tac gga att ttt gaa cga tgt aaa gag ttg 307

Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg Cys Lys Glu Leu

55

60

65

gta gaa gca gga tat gat gtc agg caa cca gat aaa gaa aat gtg tcg 355

Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Ser

70

75

80

ctt ctt cat tgg gct gct att aac aac aga ctg gat ctt gta aag ttt 403

170/754

Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp Leu Val Lys Phe
85 90 95 100

tat att tca aaa ggt gct gtt gta gat cag ttg ggt gga gat tta aat 451
Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly Gly Asp Leu Asn
105 110 115

tca act cct ctt cac tgg gcc atc cga caa gga cat tta cct atg gtc 499
Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His Leu Pro Met Val
120 125 130

ata tta tta ctc cag cat ggt gca gac ccc act ctt att gat gga gag 547
Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu Ile Asp Gly Glu
135 140 145

gga ttc agc agc atc cac ctg gca gta ttg ttt caa cac atg cct att 595
Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln His Met Pro Ile
150 155 160

ata gca tat ctc atc tca aag gga cag agt gtg aat atg aca gat gta 643
Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn Met Thr Asp Val
165 170 175 180

aat ggg cag aca cct ctc atg tta tca gct cac aaa gta att ggg cca 691
Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys Val Ile Gly Pro
185 190 195

gaa cca act gga ttt ctt tta aag ttt aat cct tct ctc aat gtg gtt 739
Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser Leu Asn Val Val

200	205	210	
gat aaa ata cac caa aac act cca ctt cac tgg gca gtt gca gca gga			787
Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala Val Ala Ala Gly			
215	220	225	
aat gtt aat gca gtt gat aag ctt ttg gaa gct ggt tct agc ctg gat			835
Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly Ser Ser Leu Asp			
230	235	240	
atc cag aat gtt aag gga gaa aca cct ctt gat atg gct cta caa aac			883
Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met Ala Leu Gln Asn			
245	250	255	260
aaa aat cag ctc att att cat atg cta aaa aca gaa gcc aaa atg aga			931
Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu Ala Lys Met Arg			
265	270	275	
gcc aac caa aag ttc aga ctt tgg agg tgg ctg cag aaa tgc gag ctc			979
Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln Lys Cys Glu Leu			
280	285	290	
ttc ctg ctg ctg atg ctt tct gtg att acc atg tgg gct att gga tac			1027
Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp Ala Ile Gly Tyr			
295	300	305	
ata ttg gac ttc aat tca gat tct tgg ctt tta aaa gga tgt ctt cta			1075
Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys Gly Cys Leu Leu			
310	315	320	

gta aca ctg ttt ttt ctg aca tct ttg ttt cca agg ttc ttg gtt ggg 1123
Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg Phe Leu Val Gly
325 330 335 340

tat aag aac ctt gta tac tta cca aca gcc ttt ctg cta agt tct gtt 1171
Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu Leu Ser Ser Val
345 350 355

ttt tgg ata ttt atg act tgg ttc atc tta ttt ttt cct gat tta gca 1219
Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe Pro Asp Leu Ala
360 365 370

gga gcc cct ttc tat ttc agt ttc att ttc agc ata gta gcc ttt cta 1267
Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile Val Ala Phe Leu
375 380 385

tac ttt ttc tat aag act tgg gca act gat cca ggc ttc act aag gct 1315
Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly Phe Thr Lys Ala
390 395 400

tct gaa gaa gaa aag aaa gtg aat atc atc acc ctt gca gaa act ggc 1363
Ser Glu Glu Glu Lys Lys Val Asn Ile Ile Thr Leu Ala Glu Thr Gly
405 410 415 420

tct ctg gac ttc aga aca ttt tgt aca tca tgt ctt ata agg aag cca 1411
Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu Ile Arg Lys Pro
425 430 435

tta agg tca ctc cac tgc cat gta tgc aac tgc tgt gtg gct cga tat 1459
 Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys Val Ala Arg Tyr

440

445

450

gat caa cac tgc ctg tgg act gga cgg tgc ata ggt ttt ggc aac cat 1507
 Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly Phe Gly Asn His

455

460

465

cac tat tac ata ttc ttc ttg ttt ttc ctt tcc atg gta tgt ggc tgg 1555
 His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met Val Cys Gly Trp

470

475

480

att ata tat gga tct ttc atc tat ttg tcc agt cat tgt gcc aca aca 1603
 Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His Cys Ala Thr Thr

485

490

495

500

ttc aaa gaa gat gga tta tgg act tac ctc aat cag att gtg gcc tgt 1651
 Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln Ile Val Ala Cys

505

510

515

tcc cct tgg gtt tta tat atc ttg atg cta gca act ttc cat ttc tca 1699
 Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr Phe His Phe Ser

520

525

530

tgg tca aca ttt tta tta tta aat caa ctc ttt cag att gcc ttt ctg 1747
 Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln Ile Ala Phe Leu

535

540

545

ggc ctg acc tcc cat gag aga atc agc ctg cag aag cag agc aag cat 1795

Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys Gln Ser Lys His
550 555 560

atg aaa cag acg ttg tcc ctc agg aag aca cca tac aat ctt gga ttc 1843
Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr Asn Leu Gly Phe
565 570 575 580

atg cag aac ctg gca gat ttc ttt cag tgt ggc tgc ttt ggc ttg gtg 1891
Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys Phe Gly Leu Val
585 590 595

aag ccc tgt gtg gta gat tgg aca tca cag tac acc atg gtc ttt cac 1939
Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr Met Val Phe His
600 605 610

cca gcc agg gag aag gtt ctt cgc tca gta tgaagaaaag caacccaaaa 1989
Pro Ala Arg Glu Lys Val Leu Arg Ser Val
615 620

ctctcaatct gatttgtttt tgtttatgtc gatgccctgt agtttgaaag tgaagtaaag 2049

atttagaatt cacctaagtc caaaggaaaa cacgtggttt ttaaagccat taggtaaaaa 2109

aagttctcaa taaaggcatt acaatttttt aggttttagaa agatggactt ttctgataaa 2169

tcttggcaga catctaaaaa aaaaaccata tttttcacia gaaaatgcaa gttacttttt 2229

ttggaaataa tactcactga ttatggataa aatggaatat tttcagatac tatattggct 2289

gtttcaaaat agtactattc tttaaacttg taatTTTTgc taagttattt gtctttgttg 2349

tatctataaa tatgtaaaaa atatttaa atagtgacct gttttgcttt cacactta at 2409

aaaaaatttt tttttgt 2426

<210> 55

<211> 257

<212> PRT

<213> Homo sapiens

<400> 55

Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met

1 5 10 15

Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe

20 25 30

Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro

35 40 45

Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu

50 55 60

Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe Ala Leu

65 70 75 80

Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr Ile Gly

	85	90	95
Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr Ser Arg			
	100	105	110
Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly Ala Gly			
	115	120	125
Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser Thr Gly			
	130	135	140
Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser Leu Gln			
	145	150	155
			160
His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro Gly Gly			
	165	170	175
Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu Ala Leu			
	180	185	190
Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile Leu Ala			
	195	200	205
Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val Ala Tyr			
	210	215	220
Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys Leu Leu			
	225	230	235
			240

Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala Thr Asp

245

250

255

Gly

<210> 56

<211> 1520

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (10)..(780)

<400> 56

tttcccaag atg gcg tcg aag ata ggt tcg aga cgg tgg atg ttg cag ctg 51

Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu

1

5

10

atc atg cag ttg ggt tcg gtg ctg ctc aca cgc tgc ccc ttt tgg ggc 99

Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly

15

20

25

30

tgc ttc agc cag ctc atg ctg tac gct gag agg gct gag gca cgc cgg 147

Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg

35

40

45

aag ccc gac atc cca gtg cct tac ctg tat ttc gac atg ggg gca gcc 195
 Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala
 50 55 60

gtg ctg tgc gct agt ttc atg tcc ttt ggc gtg aag cgg cgc tgg ttc 243
 Val Leu Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe
 65 70 75

gcg ctg ggg gcc gca ctc caa ttg gcc att agc acc tac gcc gcc tac 291
 Ala Leu Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr
 80 85 90

atc ggg ggc tac gtc cac tac ggg gac tgg ctg aag gtc cgt atg tac 339
 Ile Gly Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr
 95 100 105 110

tcg cgc aca gtt gcc atc atc ggc ggc ttt ctt gtg ttg gcc agc ggt 387
 Ser Arg Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly
 115 120 125

gct ggg gag ctg tac cgc cgg aaa cct cgc agc cgc tcc ctg cag tcc 435
 Ala Gly Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser
 130 135 140

acc ggc cag gtg ttc ctg ggt atc tac ctc atc tgt gtg gcc tac tca 483
 Thr Gly Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser
 145 150 155

ctg cag cac agc aag gag gac cgg ctg gcg tat ctg aac cat ctc cca 531

Leu Gln His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro

160

165

170

gga ggg gag ctg atg atc cag ctg ttc ttc gtg ctg tat ggc atc ctg 579

Gly Gly Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu

175

180

185

190

gcc ctg gcc ttt ctg tca ggc tac tac gtg acc ctc gct gcc cag atc 627

Ala Leu Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile

195

200

205

ctg gct gta ctg ctg ccc cct gtc atg ctg ctc att gat ggc aat gtt 675

Leu Ala Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val

210

215

220

gct tac tgg cac aac acg cgg cgt gtt gag ttc tgg aac cag atg aag 723

Ala Tyr Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys

225

230

235

ctc ctt gga gag agt gtg ggc atc ttc gga act gct gtc atc ctg gcc 771

Leu Leu Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala

240

245

250

act gat ggc tgagttttat ggcaagaggc tgagatgggc acagggagcc 820

Thr Asp Gly

255

actgagggtc accctgcctt cctccttgct ggcccagctg ctgtttatatt atgctttttg 880

gtctgtttgt ttgatctttt gcttttttaa aattgttttt tgcagttaag aggcagctca 940
 tttgtccaaa tttctgggct cagcgcttgg gagggcagga gccctggcac taatgctgta 1000
 caggtttttt tcctgttagg agagctgagg ccagctgccc actgagtctc ctgtccctga 1060
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 gggatatcca ggggcagaaa cagtaccggc tctctgtcac tcaccttgag agtagagcag 1360
 accctgttct gctctgggct gtgaaggggt ggagcaggca gtggccagct ttgcccttcc 1420
 tgctgtctct gtttctagct ccatggttgg cctggtgggg gtggagttcc ctcccaaaca 1480
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<210> 57

<211> 107

<212> PRT

<213> Homo sapiens

<400> 57

Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp Ile Gln
1 5 10 15

Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys Asp Lys
20 25 30

Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln Val Glu
35 40 45

Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu Arg Phe
50 55 60

Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp Ser Ile
65 70 75 80

Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met Arg His
85 90 95

Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val
100 105

<210> 58

<211> 1496

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (9).. (329)

<400> 58

ctaccagg atg gct ctc ttc gct ggt ggc aaa ctg cgt gtg cat ctc gac 50

Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp

1

5

10

atc cag gtt ggg gag cat gcc aac aac tac cct gag att gct gca aaa 98

Ile Gln Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys

15

20

25

30

gat aag ctg acg gag cta cag ctc cgc gcc cgc cag ttg ctt gat cag 146

Asp Lys Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln

35

40

45

gtg gaa cag att cag aag gag cag gat tac caa agg tat cgt gaa gag 194

Val Glu Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu

50

55

60

cgc ttc cga ctg acg agc gag agc acc aac cag agg gtc cta tgg tgg 242

Arg Phe Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp

65

70

75

tcc att gct cag act gtc atc ctc atc ctc act ggc atc tgg cag atg 290

Ser Ile Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met

80

85

90

cgt cac ctc aag agc ttc ttt gag gcc aag aag ctg gtg tagtgccctc 339

Arg His Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val

tttgatgac ccttcctttt tacctcattt atttggtact ttccccacac agtcctttat 399
ccacctggat ttttagggaa aaaaaatgaa aaagaataag tcacattggt tccatggcca 459
caaaccattc agatcagcca ctgtctgacc ctggttctta aggacacatg acattagtc 519
aatctttcaa aatcttgtct tagggcttgt gaggaatcag aactaaccca ggactcagtc 579
ctgcttcttt tgccctgagt gattttcttc tgtttttcac taaataagca aatgaaaact 639
ctctccatta ccttctgctt tctctttgtc cacttacgca gtaggtgact ggcatgtgcc 699
acagagcagg cccctgcctca ctgtctgctg gtcagttctg ggttcactta atggctttgt 759
gaatgtaa at aaggggcagg tcttgccct agaggattga gatgttttc tatacttag 819
aactattttt ggataaatta tatattttcc ttctagtag aagtgttact gcctgtaact 879
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taccatgttg gccaggctgg tcttagactc ctgacctcag ttgatccacc tgcctcagcc 1179

tctgcattca gtttattcac atatTTTTtg taactcccat ggcagctcct aggatttcag 1239

cggTctgtgg gccagaaagc aggcaccagg gctgacctca aggccgtatc agagggccaa 1299

gcagagttct tttggatacc tgcttttcat cccacagggc cttagagtca gaggtaaggt 1359

agcaacagag ctagaatggg gcaatgcact cttacctcc ttctcaactt ttatttaagc 1419

tgtgctaaat gttttcttca agggaaccag atttagttct ttacagaatt ttccagtga 1479

ataaaacatg ttgtaat 1496

<210> 59

<211> 272

<212> PRT

<213> Homo sapiens

<400> 59

Met Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly

1 5 10 15

Pro Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp

20 25 30

Val Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met

35 40 45

Met Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly
50 55 60

Ile Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln
65 70 75 80

Gly Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr
85 90 95

Glu Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr
100 105 110

Thr Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys
115 120 125

Val Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg
130 135 140

Glu Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu
145 150 155 160

His Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro
165 170 175

Ser Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val
180 185 190

Leu Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr
195 200 205

Tyr Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu
210 215 220

Met His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln
225 230 235 240

Tyr Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu
245 250 255

Arg Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu
260 265 270

<210> 60

<211> 1916

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (117).. (932)

<400> 60

atggtaacgg ctcggaagcc taggaggctg ggccggaggg aggcggagga accggtgttc 60

gccgccgccg ctgcttcagc ttattccttg tggectctgc gggtcctgcc tcagcc atg 119

Met

1

atg atc cac ggc ttc cag agc agc cac cgg gat ttc tgc ttc ggg ccc 167
Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly Pro

5

10

15

tgg aag ctg acg gcg tcc aag acc cac atc atg aag tcg gcg gat gtg 215
Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp Val

20

25

30

gag aaa tta gcc gat gaa tta cat atg cca tct ctc cct gaa atg atg 263
Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met Met

35

40

45

ttt gga gac aac gtt tta aga atc cag cat ggg tct ggc ttt gga att 311
Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly Ile

50

55

60

65

gag ttc aat gct aca gat gcg tta aga tgt gta aac aac tac caa gga 359
Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln Gly

70

75

80

atg ctt aaa gtg gcc tgt gct gaa gag tgg caa gaa agc agg acg gag 407
Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr Glu

85

90

95

ggc gaa cac tcc aaa gag gtt att aaa cca tat gat tgg acc tat aca 455
Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr Thr

100

105

110

aca gat tat aag gga acc tta ctt gga gaa tct ctt aag tta aag gtt 503
 Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys Val
 115 120 125

gta cct aca aca gat cat ata gat aca gaa aaa ttg aaa gcc aga gaa 551
 Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg Glu
 130 135 140 145

cag att aag ttt ttt gaa gaa gtt ctc ctt ttt gag gat gaa ctt cat 599
 Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu His
 150 155 160

gat cat gga gtt tca agc ctg agt gtg aag att aga gta atg cct tct 647
 Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro Ser
 165 170 175

agc ttt ttc ctg ctg ttg cgg ttt ttc ttg aga att gat ggg gtg ctt 695
 Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val Leu
 180 185 190

atc aga atg aat gac acg aga ctt tac cat gag gct gac aag acc tac 743
 Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr Tyr
 195 200 205

atg tta cga gaa tat acg tca cga gaa agc aaa att tct agt ttg atg 791
 Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu Met
 210 215 220 225

cat gtt cca cct tcc ctc ttc acg gaa cct aat gaa ata tcc cag tat 839

His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln Tyr
230 235 240

tta cca ata aag gaa gca gtt tgt gag aag cta ata ttt cca gaa aga 887
Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu Arg
245 250 255

att gat cct aac cca gca gac tca caa aaa agt aca caa gtg gaa 932
Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu
260 265 270

taaaatgtga tacaacatat actcactatg gaatctgact ggacaccttg gctatttgta 992

aggggttatt tttattatga gaattaattg ccttgtttat gtacagattt tctgtagcct 1052

taaaggaaaa aaaaataaag atcgttacag gcaggtttca ctcaactgct atttgtactg 1112

tctgtcttca cattcatatt ccagatttat attttctgga gttaaatttg gatgatttct 1172

aaattatcac aaagtgggac ctcagcagta gtgatgtgtg tgtctcatga gcagtgagca 1232

cagtctgcat tcatcatgaa aactatctt ctaccaggag gaggttaatg taaatcacca 1292

aatcccaatg ccttgatgact ttcataaggat tctgatcat gcatgttgat gtactggctc 1352

ttcactttgg gctttctgat gtttattcac acctttggag agttgcaact tgccacatac 1412

gaaattagtc tcatagtgtg gtgaacttca accccaaaat tttaaaaatg tatttccccc 1472

cagttttaaa ttgcctttga aatttaaaaa aaaaaattta gacttagtac cagaaccaa 1532
aatacctaga tttttggaga acttattaca tacatagaaa catgaatatg gtttaccwct 1592
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tcttgggtccc tgaatagtcc tagattactt attttgagaa ttgattgtta aaaattacag 1712
ggaattaaaa taattgcctt ttttttttta gagggtaaga gatgggtaga agagtatgcc 1772
totgaaaatt ttattagttt attcttgtgg agaataccaa gaaaatgtgt atttgcccat 1832
tgctaaatat gatatatgcc attttgtatt tatttgtccc aagtgtcttt ttttaagagg 1892
agaataaaca ataaggaatt actg 1916

<210> 61

<211> 219

<212> PRT

<213> Homo sapiens

<400> 61

Met Asn Arg Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser

1 5 10 15

Leu Thr Asp Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp

20 25 30

Lys Lys Ile Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln
35 40 45

Ile Lys Lys Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys
50 55 60

Ala Leu Arg Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp
65 70 75 80

Asn Leu Ala Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile
85 90 95

Gln Ser Leu Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly
100 105 110

Val Lys Glu Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile
115 120 125

Glu Asp Leu Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu
130 135 140

Ile Gln Glu Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu
145 150 155 160

Asp Asp Leu Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala
165 170 175

Asp Glu Asp Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile
180 185 190

Pro Glu Gly Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val
 195 200 205

Asp Glu Phe Gly Leu Pro Gln Ile Pro Ala Ser
 210 215

<210> 62

<211> 1362

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (49)..(705)

<400> 62

gttttctggt ttgctctag tgtttgggtt tcttcgcggc tgctcaag atg aac cga 57

Met Asn Arg

1

ctc ttc ggg aaa gcg aaa ccc aag gct ccg ccg ccc agc ctg act gac 105

Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser Leu Thr Asp

5

10

15

tgc att ggc acg gtg gac agt aga gca gaa tcc att gac aag aag att 153

Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp Lys Lys Ile

20	25	30	35	
tct cga ttg gat gct gag cta gtg aag tat aag gat cag atc aag aag	201			
Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln Ile Lys Lys				
40	45	50		
atg aga gag ggt cct gca aag aat atg gtc aag cag aaa gcc ttg cga	249			
Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys Ala Leu Arg				
55	60	65		
gtt tta aag caa aag agg atg tat gag cag cag cgg gac aat ctt gcc	297			
Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp Asn Leu Ala				
70	75	80		
caa cag tca ttc aac atg gaa caa gcc aat tat acc atc cag tct ttg	345			
Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile Gln Ser Leu				
85	90	95		
aag gac acc aag acc acg gtt gat gct atg aaa ctg gga gta aag gaa	393			
Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly Val Lys Glu				
100	105	110	115	
atg aag aag gca tac aag caa gtg aag atc gac cag att gag gat tta	441			
Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile Glu Asp Leu				
120	125	130		
caa gac cag cta gag gat atg atg gaa gat gca aat gaa atc caa gaa	489			
Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu Ile Gln Glu				
135	140	145		

gca ctg agt cgc agt tat ggc acc cca gaa ctg gat gaa gat gat tta 537

Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu Asp Asp Leu

150

155

160

gaa gca gag ttg gat gca cta ggt gat gag ctt ctg gct gat gaa gac 585

Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala Asp Glu Asp

165

170

175

agt tct tat ttg gat gag gca gca tct gca cct gca att cca gaa ggt 633

Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile Pro Glu Gly

180

185

190

195

gtt ccc act gat aca aaa aac aag gat gga gtt ctg gtg gat gaa ttt 681

Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val Asp Glu Phe

200

205

210

gga ttg cca cag atc cct gct tca tagatttgca tcattcaagc atatcttgta 735

Gly Leu Pro Gln Ile Pro Ala Ser

215

aaacaaacac atattatggg actaggaaat atttatcttt ccaaatttgc cataacagat 795

ttaggtttct ttccttttctt tgaaggaaag tttaattaca ttgctctttt attttttcca 855

ttaagagact cattgcttgg gaaatgcttt cttcgtacta aaatttgatt cctttttttt 915

cttatgaaaa acgaactcag tttaaaagta ttttagctc gtatgacttg ttttcattca 975

ttaataataa tttgaaataa aactaaggaa atggaatctt aaaagtctat gacagtgtaa 1035

ctctacagtc tcaaaatgac ctgataaatt gataagacaa agatgagatt attggggctg 1095

ttcatattat gattcagaat cattttctat tgtggtatta taggttggtt aaagtgatgg 1155

cctttttgat gggttttggt gtgtcttgtg aacaagtcgt tactgtgtcc attattggaa 1215

tggaattatc actactgtat catgagtggg tattttgatt ctatggttcc ctcagtatta 1275

catcttgact tgtaatcaat tatgaatatt tcttgatatt taatgtatag gacatttatt 1335

tatactcaat aaatattttt caaaagg 1362

<210> 63

<211> 622

<212> PRT

<213> Homo sapiens

<400> 63

Met Ala Asp Gly Pro Asp Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro

1 5 10 15

Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His Tyr Asn His Gly

20 25 30

Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp Asp Tyr Ser Thr

35 40 45

Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg
50 55 60

Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn
65 70 75 80

Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg Ile Asp Leu Val
85 90 95

Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln Leu Gly Gly Asp
100 105 110

Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln Gly His Leu Ser
115 120 125

Met Val Val Gln Leu Met Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp
130 135 140

Gly Glu Gly Cys Ser Cys Ile His Leu Ala Ala Gln Phe Gly His Thr
145 150 155 160

Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp Val Asp Met Met
165 170 175

Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala Tyr Arg Thr His
180 185 190

Ser Val Asp Pro Thr Arg Leu Leu Leu Thr Phe Asn Val Ser Val Asn

195	200	205
Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His Trp Ala Val Leu		
210	215	220
Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn		
225	230	235 240
Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys		
245	250	255
Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln Glu Ala Arg Gln		
260	265	270
Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp		
275	280	285
Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro Phe Leu Val Ile		
290	295	300
Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile		
305	310	315 320
Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val Gln Phe Leu Ser		
325	330	335
Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu Pro Leu Gly Ile		
340	345	350

Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp Phe Phe Trp Phe
355 360 365

Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro Phe Leu Ala Asn
370 375 380

Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro
385 390 395 400

Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys Thr Ile Val Glu
405 410 415

Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys
420 425 430

Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly Val Cys Asn Arg
435 440 445

Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val Gly Asn Cys Val
450 455 460

Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu
465 470 475 480

Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu
485 490 495

His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr
500 505 510

Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met Phe Leu Asn Ser
515 520 525

Val Phe His Phe Met Trp Val Ala Val Leu Leu Met Cys Gln Met Tyr
530 535 540

Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg Met Asn Ala Arg
545 550 555 560

Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile Glu Ser Pro Phe
565 570 575

Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys
580 585 590

Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr Arg Gln Tyr Thr
595 600 605

Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln Leu Val
610 615 620

<210> 64

<211> 2948

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (14)..(1879)

<400> 64

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Met Ala Asp Gly Pro Asp Glu Tyr Asp Thr Glu Ala

1

5

10

ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc caa agc cat 97

Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His

15

20

25

tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act cat att gat 145

Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp

30

35

40

gat tac agc aca tgg gac ata gtc aag gct aca caa tat gga ata tat 193

Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr

45

50

55

60

gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta cgg caa ccg 241

Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro

65

70

75

gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc aat aac aga 289

Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg

80

85

90

ata gat tta gtc aaa tac tat att tcg aaa ggt gct att gtg gat caa 337

Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln	
95	100
105	
ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc aca aga caa	385
Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln	
110	115
120	
ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt gca gat cct	433
Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly Ala Asp Pro	
125	130
135	140
tca tta att gat gga gaa gga tgt agc tgt att cat ctg gct gct cag	481
Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu Ala Ala Gln	
145	150
155	
ttc gga cat acc tca att gtt gct tat ctc ata gca aaa gga cag gat	529
Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp	
160	165
170	
gta gat atg atg gat cag aat gga atg acg cct tta atg tgg gca gca	577
Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala	
175	180
185	
tat aga aca cat agt gtg gat cca act aga ttg ctt tta aca ttc aat	625
Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu Thr Phe Asn	
190	195
200	
gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act gct ctg cat	673
Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His	

205	210	215	220	
tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt ctt ctg gaa	721			
Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Leu Glu				
225	230	235		
gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa tca gcg ctt	769			
Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu				
240	245	250		
gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac cac tta caa	817			
Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln				
255	260	265		
gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc ctt aga aag	865			
Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys				
270	275	280		
ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta gga act cct	913			
Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro				
285	290	295	300	
ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta aat att gat	961			
Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp				
305	310	315		
tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg gct aca gta	1009			
Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val				
320	325	330		

cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat agt gca ttg 1057

Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu

335

340

345

ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat gtg acg tgg 1105

Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp

350

355

360

ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc cat ctt cca 1153

Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro

365

370

375

380

ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga aaa tct tgg 1201

Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp

385

390

395

aaa tca gat cca ggg att att aaa gca aca gaa gag caa aag aaa aag 1249

Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys

400

405

410

aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc agt ata ttc 1297

Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe

415

420

425

tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa cat tgt ggt 1345

Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly

430

435

440

gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc cca tgg gtg 1393
Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val
445 450 455 460

ggt aac tgt gta ggt gca ggc aac cat aga tat ttt atg ggc tac cta 1441
Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu
465 470 475

ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt tgt ata tct 1489
Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser
480 485 490

tac tgg gga ctc cac tgt gag acc act tac acc aag gat gga ttt tgg 1537
Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp
495 500 505

aca tac att act cag att gcc acg tgt tca cct tgg atg ttt tgg atg 1585
Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met
510 515 520

ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta tta ctc atg 1633
Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val Leu Leu Met
525 530 535 540

tgt cag atg tac cag ata tca tgt tta ggt att act aca aat gaa aga 1681
Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg
545 550 555

atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca acg tct att 1729

Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile
560 565 570

gaa agc cca ttc aac cat gga tgt gta aga aat att ata gac ttc ttt 1777
Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe
575 580 585

gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg gac tgg acc 1825
Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr
590 595 600

agg cag tat aca ata gaa tat gac caa ata tca gga tct ggg tac cag 1873
Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln
605 610 615 620

ctg gtg tagcgacatc ttatcctatg aagcatattg ctgagtgggtg cctgaaaatt 1929
Leu Val

gtgtctgtcc gtgtctttct cacactcgaa tccacatcct ttgaacaaga gcatgctatg 1989

tgtagggcta atgggtgaatt ttacagtctt tttttcaaca cttttattaa caaaagtaaa 2049

catggacaga acacactgcc atttctggga agagtaaaga tgataaaaaa taattttaat 2109

ggttcttaat gtggaaattc acaacatact caacttttgg gttttgttct cacagtatgt 2169

ttcacaaaaa aagggtaaac ttattctatt gacagacatg gtgtactgat cagaaatggt 2229

cagttttaac taaaactaaa tttatgttat ttggctaaat gttatgatgc agtctagtag 2289

gagtattgca tctaattcca ggagcattgt ttttaagttga ttgactagtt attatgtaca 2349
 tttcagaatg tacacataaa tactgtgatg aaaatcatgt gattgggatc tactgtgatg 2409
 ttgtcttcaa aggcaggaga aaataatggt cacaataaaa tgtgctaaca atgttttggt 2469
 tctatcagct gttgcaatgc tgatatattt ctagttcagt gaaataattt gtagtaacct 2529
 tactctgagg ttttacggtc tgataatgaa gcacttgcac gagtatagta agtcatgttt 2589
 ttttgttcaa atttaaaagc cctgctaatt gcatgacaca ccacatagaa tgtatactag 2649
 cagatactat ccagtgaagc ataaattaga atttaatttg atgttcaaaa acagttccat 2709
 ttttaagggt taagggtgga ttttcaagaa aaggcagaac aaataatgca aaattctcag 2769
 taatagtgat acatggatat acttcctttt aaattctcag ctgcaaaata attgtagaca 2829
 aaataatggc atttaactaa agatggagca tgatctgtgt acatagcaca tgtgaataaa 2889
 agaaaagctg acagtatatt ctggtttcaa taaaatgacc tatcagaaag tagaatttc 2948

<210> 65

<211> 632

<212> PRT

<213> Homo sapiens

<400> 65

Met Gln Arg Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp
1 5 10 15

Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu
20 25 30

Ile Lys Pro Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly
35 40 45

Arg Lys Thr His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala
50 55 60

Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly
65 70 75 80

Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp
85 90 95

Ala Ala Ile Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys
100 105 110

Gly Ala Ile Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu
115 120 125

His Trp Ala Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met
130 135 140

Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys

145	150	155	160
Ile His Leu Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu			
	165	170	175
Ile Ala Lys Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr			
	180	185	190
Pro Leu Met Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg			
	195	200	205
Leu Leu Leu Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His			
	210	215	220
Lys Asn Thr Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val			
225	230	235	240
Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile			
	245	250	255
Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp			
	260	265	270
Met Ile Asn His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn			
	275	280	285
Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys			
	290	295	300

Val Met Leu Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile
305 310 315 320

Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly
325 330 335

Gly Val Trp Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His
340 345 350

Ser Met His Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe
355 360 365

Trp Met Tyr Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe
370 375 380

Leu Phe Ile His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr
385 390 395 400

Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr
405 410 415

Glu Glu Gln Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser
420 425 430

Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val
435 440 445

Arg Ser Lys His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp
450 455 460

His His Cys Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg
465 470 475 480

Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met
485 490 495

Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr
500 505 510

Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser
515 520 525

Pro Trp Met Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp
530 535 540

Val Ala Val Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly
545 550 555 560

Ile Thr Thr Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys
565 570 575

Val Thr Thr Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg
580 585 590

Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro
595 600 605

Val Ile Val Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile
211/754

610

615

620

Ser Gly Ser Gly Tyr Gln Leu Val

625

630

<210> 66

<211> 4715

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (108).. (2003)

<400> 66

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cctccgcctc gcccgagccc cgggaggggtg aaacgctttc tcccagc atg cag cgg 116

Met Gln Arg

1

gag gag gga ttt aac acc aag atg gcg gac ggc ccg gat gag tac gat 164

Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp Glu Tyr Asp

5

10

15

acc gaa gcg ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc 212

Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro

20

25

30

35

caa agc cat tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act 260
Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr

40 45 50

cat att gat gat tac agc aca tgg gac ata gtc aag gct aca caa tat 308
His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr

55 60 65

gga ata tat gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta 356
Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val

70 75 80

cgg caa ccg gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc 404
Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile

85 90 95

aat aac aga ata gat tta gtc aaa tac tat att tcg aaa ggt gct att 452
Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile

100 105 110 115

gtg gat caa ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc 500
Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala

120 125 130

aca aga caa ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt 548
Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly

135 140 145

gca gat cct tca tta att gat gga gaa gga tgt agc tgt att cat ctg 596
 Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu

150

155

160

gct gct cag ttc gga cat acc tca att gtt gct tat ctc ata gca aaa 644
 Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys

165

170

175

gga cag gat gta gat atg atg gat cag aat gga atg acg cct tta atg 692
 Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met

180

185

190

195

tgg gca gca tat aga aca cat agt gtg gat cca act aga ttg ctt tta 740
 Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu

200

205

210

aca ttc aat gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act 788
 Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr

215

220

225

gct ctg cat tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt 836
 Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu

230

235

240

ctt ctg gaa gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa 884
 Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu

245

250

255

tca gcg ctt gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac 932

Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn
 260 265 270 275

cac tta caa gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc 980
 His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe
 280 285 290

ctt aga aag ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta 1028
 Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu
 295 300 305

gga act cct ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta 1076
 Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu
 310 315 320

aat att gat tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg 1124
 Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp
 325 330 335

gct aca gta cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat 1172
 Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His
 340 345 350 355

agt gca ttg ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat 1220
 Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr
 360 365 370

gtg acg tgg ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc 1268
 Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile

375	380	385	
cat ctt cca ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga	1316		
His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly			
390	395	400	
aaa tct tgg aaa tca gat cca ggg att att aaa gca aca gaa gag caa	1364		
Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln			
405	410	415	
aag aaa aag aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc	1412		
Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu			
420	425	430	435
agt ata ttc tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa	1460		
Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys			
440	445	450	
cat tgt ggt gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc	1508		
His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys			
455	460	465	
cca tgg gtg ggt aac tgt gta ggt gca ggc aac cat aga tat ttt atg	1556		
Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met			
470	475	480	
ggc tac cta ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt	1604		
Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly			
485	490	495	

tgt ata tct tac tgg gga ctc cac tgt gag acc act tac acc aag gat 1652
Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp
500 505 510 515

gga ttt tgg aca tac att act cag att gcc acg tgt tca cct tgg atg 1700
Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met
520 525 530

ttt tgg atg ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta 1748
Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val
535 540 545

tta ctc atg tgt cag atg tac cag ata tca tgt tta ggt att act aca 1796
Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr
550 555 560

aat gaa aga atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca 1844
Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr
565 570 575

acg tct att gaa agc cca ttc aac cat gga tgt gta aga aat att ata 1892
Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile
580 585 590 595

gac ttc ttt gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg 1940
Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val
600 605 610

gac tgg acc agg cag tat aca ata gaa tat gac caa ata tca gga tct 1988

Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser

615

620

625

ggg tac cag ctg gtg tagcgacatc ttatcctatg aagcatattg ctgagtgtg 2043

Gly Tyr Gln Leu Val

630

cctgaaaatt gtgtctgtcc gtgtctttct cacactcgaa tccacatcct ttgaacaaga 2103

gcatgctatg tgtagggcta atgggtgaatt ttacagtctt tttttcaaca cttttattaa 2163

caaaagtaaa catggacaga acacactgcc atttctggga agagtaaaga tgataaaaaa 2223

taattttaat gggtcttaat gtggaaattc acaacatact caacttttgg gttttgttct 2283

cacagtattt ttcacaaaaa aagggtaaac ttattctatt gacagacatg gtgtactgat 2343

cagaaatggt cagttttaac taaaactaaa tttatgttat ttggctaaat gttatgatgc 2403

agtctagtac gagtattgca tctaattcca ggagcattgt ttaagtga ttgactagtt 2463

attatgtaca tttcagaatg tacacataaa tactgtgatg aaaatcatgt gattgggatc 2523

tactgtgatg ttgtcttcaa aggcaggaga aaataatggt cacaataaaa tgtgctaaca 2583

atgttttggt tctatcagct gttgcaatgc tgatatatct ctagttcagt gaaataattt 2643

gtagtaacct tactctgagg ttttacggtc tgataatgaa gcacttgcac gagtatagta 2703

agtcatgttt ttttgttcaa atttaaaagc cctgctaatt gcatgacaca ccacatagaa 2763

tgtatactag cagatactat ccagtgaagc ataaattaga atttaatttg atgttcaaaa 2823

acagttccat ttttaagggt taagggtgga ttttcaagaa aaggcagaac aaataatgca 2883

aaattctcag taatagtgat acatggatat acttcctttt aaattctcag ctgcaaaata 2943

attgtagaca aaataatggc atttaactaa agatggagca tgatctaagt acatagcaca 3003

tgtgaataaa agaaaagctg acagtatatt ctggtttcaa taaaatgacc tatcagaaag 3063

tagaatttca tccccaaagag tatttcagtt tatccaatat tgagtaagtt ctgaaacagt 3123

tttagaaaaa attttctttt tgttaaatgt gatgcactga tcaatttttg tcacagcatt 3183

ttcatacctt catggtggac tactagtcac tgcttcata aatattgttt acagggtgag 3243

atttggttta ttcattctaa gtgctgtagc aaactgtggt tcgagcaacc tgtgggaaat 3303

ctgtgagagg gaatggggtg ggagatgtgg gggaatgggtg gtcagactga tgacagatcc 3363

tagaccaatg taaagaatgt gtatctgtat ataaataatt tatcaaatag ttttctcttt 3423

gtgtctgtgt tagtgttttt aaagctgctc atttcatttt gtccaaccaa aaagaaaagg 3483

gagataacta atgagcttct agtgatgttc aaaattgctg ttaataggca ttataccctg 3543

caagttcact gcatgtctga tgcttggttaa aactagtctt ccctgtaaaa tgcagattac 3603

aggtattaaa gcaatctagt ggtatacccg ccccttgcct tagtaagagg agcagtgaaa 3663

tgtatatagt tgatgttcag tatttccaag taccattttt atatagtagc ttatttgacc 3723

ataagtcaca catcaaaaaa agattaccct tagtgtatgt gttttaatat tagaaaattg 3783

gcatatgtac tttatttttg aaaagggaag agatgggtgt ggggtggcaa tagcattgtg 3843

ccattttgtc atagaatgta aaaattgggt aactttacaa atgtcagcta gttttgacta 3903

ctaattgggg gaaatttttag ataattttta aattcaaagt tatttataaa atgctagaat 3963

ttgttttaat tttttgtatt ttgagccact tcacatgaag actcagttgc atttttatcg 4023

aatacatttt tatcaacagt taaagactat ggtgggtttt tcagagtttg gctaagaatg 4083

ttgttaccat cttctttgtt tgtggtacaa tattttcagt gcaaaagaga tgtcattcag 4143

ttaaaaagac aaacctctag atgtgtaatt acatggaaaa tactagcaat gtgaatgctt 4203

ttgtagtaac catctttag tagctgtgaa atctataact cagaaatggt cagatgggtca 4263

ggagccagct atgcagcagt ataccatctg ttttaattatt ttgtaggtcc tgtgtgtgga 4323

accaactata aaccagttc taaagttgtg tatgatgggt aacctttggg aatagttctt 4383

atcaacttaa ttggatactt ttagcaaata ggaacttaat tctcagcact gaacatgaat 4443

tacttccttg gagttttttt tcattcatat ttttgttggt tccaggaatt tatttgatat 4503

taatgggagt aaaacagcat cattgtactt aagctatgga tgtttttatt ttatatatttc 4563

tttattttata actgtgccaa gtattatttt gctacttacc gtgttattct gtggaaagaa 4623

aaacctgtaa agtgtttaat aaattagccc tccttacata aattaaatgt caaaattttg 4683

taaaatatta atcagaataa atactgactc tt 4715

<210> 67

<211> 498

<212> PRT

<213> Homo sapiens

<400> 67

Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu

1 5 10 15

Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp

20 25 30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu

35 40 45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly

50 55 60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr
65 70 75 80

Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr
85 90 95

Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala
100 105 110

Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met
115 120 125

Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg
130 135 140

Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln
145 150 155 160

Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp
165 170 175

Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly
180 185 190

Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln
195 200 205

Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn

210	215	220
Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile		
225	230	235 240
Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala		
245	250	255
Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val		
260	265	270
His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr		
275	280	285
Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro		
290	295	300
Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu		
305	310	315 320
Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu		
325	330	335
Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu		
340	345	350
Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr		
355	360	365

Met His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr
370 375 380

Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser
385 390 395 400

Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser
405 410 415

Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe
420 425 430

Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu
435 440 445

Gly Gln Met Arg Pro Glu Gly Val Gly Leu Pro Ala Glu Val Thr Gln
450 455 460

Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp
465 470 475 480

Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe
485 490 495

Ser Cys

<210> 68

<211> 1902

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22)..(1515)

<400> 68

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gaaggaggga atgactccag g atg gcc cgg ctg gaa gtg att gaa ctg cct 51
                Met Ala Arg Leu Glu Val Ile Glu Leu Pro
                        1                5                10
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```
cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac 99
His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His
                15                20                25
```

```
gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att 147
Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile
                30                35                40
```

```
ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg 195
Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val
                45                50                55
```

```
cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc 243
His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly
                60                65                70
```

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa 291
 Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu
 75 80 85 90

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct 339
 Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro
 95 100 105

gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg 387
 Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg
 110 115 120

act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag 435
 Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu
 125 130 135

cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc 483
 His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly
 140 145 150

ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac 531
 Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn
 155 160 165 170

tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag 579
 Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln
 175 180 185

gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg 627
Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val
190 195 200

acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg 675
Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val
205 210 215

cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct 723
Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro
220 225 230

ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg 771
Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu
235 240 245 250

gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc 819
Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala
255 260 265

cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag 867
Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys
270 275 280

ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac 915
Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp
285 290 295

ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca 963

Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro
 300 305 310

gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc 1011
 Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu
 315 320 325 330

aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc 1059
 Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly
 335 340 345

tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg 1107
 Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr
 350 355 360

cac acc ctg aac agc acg atg cac gag tac aag atc caa ggc ctc tca 1155
 His Thr Leu Asn Ser Thr Met His Glu Tyr Lys Ile Gln Gly Leu Ser
 365 370 375

tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc 1203
 Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly
 380 385 390

act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac 1251
 Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp
 395 400 405 410

ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc 1299
 Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg

415	420	425	
tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc	1347		
Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile			
430	435	440	
tcc agg tgg att gtt gag ggg cag atg aga cct gaa ggt gtt gga tta	1395		
Ser Arg Trp Ile Val Glu Gly Gln Met Arg Pro Glu Gly Val Gly Leu			
445	450	455	
cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca	1443		
Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala			
460	465	470	
aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc	1491		
Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser			
475	480	485	490
cag aaa ctt tgg gaa ttc tct tgt tagttggtta gttttactgt aattttctat	1545		
Gln Lys Leu Trp Glu Phe Ser Cys			
495			
aaagaattca tatcatctgt taatggcgac agtttttggt tcttccttg aattttttat	1605		
attctttctt tctctttttt gtttcttctt ctttgagtat tttgtaatct tactgggagg	1665		
gctaaagcgt cttctatcat atcgaattgg gacaatgata gaagacaatc tttgttttgt	1725		
cactctaaag aaattattgt aagattttat catcaggtat gacatttaca ccattgatgt	1785		

aggcttttta aaaaatatat ccagcctgta ttgggttaag atgattcttt tctgacctg 1845

atttcctagg agttggtttt ttttttttta aagcataaat aaatttaatt gcatcag 1902

<210> 69

<211> 498

<212> PRT

<213> Homo sapiens

<400> 69

Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu

1 5 10 15

Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp

20 25 30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu

35 40 45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly

50 55 60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr

65 70 75 80

Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr

85 90 95

Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala
100 105 110

Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met
115 120 125

Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg
130 135 140

Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln
145 150 155 160

Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp
165 170 175

Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly
180 185 190

Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln
195 200 205

Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn
210 215 220

Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile
225 230 235 240

Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala
231/754

245	250	255
Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val		
260	265	270
His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr		
275	280	285
Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro		
290	295	300
Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu		
305	310	315
Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu		
325	330	335
Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu		
340	345	350
Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr		
355	360	365
Thr His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr		
370	375	380
Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser		
385	390	395
		400

Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser
405 410 415

Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe
420 425 430

Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu
435 440 445

Gly Gln Met Arg His Gln Gly Val Gly Leu Pro Ala Glu Val Thr Gln
450 455 460

Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp
465 470 475 480

Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe
485 490 495

Ser Cys

<210> 70

<211> 1902

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22).. (1515)

<400> 70

gaaggaggga atgactccag g atg gcc cgg ctg gaa gtg att gaa ctg cct 51
Met Ala Arg Leu Glu Val Ile Glu Leu Pro
1 5 10

cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac 99
His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His
15 20 25

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att 147
Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile
30 35 40

ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg 195
Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val
45 50 55

cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc 243
His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly
60 65 70

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa 291
Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu
75 80 85 90

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct 339
Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro

95	100	105	
gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg			387
Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg			
110	115	120	
act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag			435
Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu			
125	130	135	
cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc			483
His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly			
140	145	150	
ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac			531
Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn			
155	160	165	170
tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag			579
Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln			
175	180	185	
gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg			627
Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val			
190	195	200	
acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg			675
Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val			
205	210	215	

cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct	723
Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro	
220 225 230	
ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg	771
Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu	
235 240 245 250	
gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc	819
Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala	
255 260 265	
cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag	867
Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys	
270 275 280	
ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac	915
Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp	
285 290 295	
ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca	963
Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro	
300 305 310	
gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc	1011
Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu	
315 320 325 330	

aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc 1059
 Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly

335 340 345

tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg 1107
 Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr

350 355 360

cac acc ctg aac agc acg acg cac gag tac aag atc caa ggc ctc tca 1155
 His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys Ile Gln Gly Leu Ser

365 370 375

tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc 1203
 Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly

380 385 390

act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac 1251
 Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp

395 400 405 410

ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc 1299
 Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg

415 420 425

tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc 1347
 Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile

430 435 440

tcc agg tgg att gtt gag ggg cag atg aga cat caa ggt gtt gga tta 1395

Ser Arg Trp Ile Val Glu Gly Gln Met Arg His Gln Gly Val Gly Leu

445

450

455

cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca 1443

Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala

460

465

470

aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc 1491

Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser

475

480

485

490

cag aaa ctt tgg gaa ttc tct tgt tagttggtta gttttactgt aattttctat 1545

Gln Lys Leu Trp Glu Phe Ser Cys

495

aaagaattca tatcatctgt taatggcgac agtttttggt tcttcctttg aattttttat 1605

attctttctt tctctttttt gtttcttctt ctttgagtat tttgtaatct tactgggagg 1665

gctaaagcgt cttctatcat atcgaattgg gacaatgata gaagacaatc tttgttttgt 1725

cactctaaag aaattattgt aagattttat catcaggtat gacatttaca ccattgatgt 1785

aggtttttta aaaaatatat ccagcctgta ttgggttaag atgattcttt tctgatcctg 1845

atttcctagg agttggtttt ttttttttta aagcataaat aaatttaatt gcatcag 1902

<211> 245

<212> PRT

<213> Homo sapiens

<400> 71

Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser Met His

1 5 10 15

Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser Met Thr

20 25 30

Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile Leu Thr

35 40 45

Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His Arg Pro

50 55 60

Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg Leu Gly

65 70 75 80

Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser Pro Pro

85 90 95

Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile Ala Asp

100 105 110

Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe Ser Tyr

115 120 125

Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys Val Ala
130 135 140

Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu Ala Glu
145 150 155 160

Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn Gly Lys
165 170 175

Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile Glu Gly
180 185 190

Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly Thr Val
195 200 205

Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile Val Arg
210 215 220

Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val Leu Gly
225 230 235 240

Gln Trp Ile Gln Arg
245

<210> 72

<211> 1551

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (127).. (861)

<400> 72

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ccaagccccg ccgacgcggg gcaccggagc cagccccgca gcgggtcccg cctgtctgtc 120

acgctg atg ccc gtg cag ctg tct gag cac ccg gaa tgg aat gag tct 168

Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser

1

5

10

atg cac tcc ctc cgg atc agt gtg ggg ggc ctt cct gtg ctg gcg tcc 216

Met His Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser

15

20

25

30

atg acc aag gcc gcg gac ccc cgc ttc cgc ccc cgc tgg aag gtg atc 264

Met Thr Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile

35

40

45

ctg acg ttc ttt gtg ggt gct gcc atc ctc tgg ctg ctc tgc tcc cac 312

Leu Thr Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His

50

55

60

cgc ccg gcc ccc ggc agg ccc ccc acc cac aat gca cac aac tgg agg 360

Arg Pro Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg

65

70

75

ctc ggc cag gcg ccc gcc aac tgg tac aat gac acc tac ccc ctg tct 408

Leu Gly Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser

80

85

90

ccc cca caa agg aca ccg gct ggg att cgg tat cga atc gca gtt atc 456

Pro Pro Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile

95

100

105

110

gca gac ctg gac aca gag tca agg gcc caa gag gaa aac acc tgg ttc 504

Ala Asp Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe

115

120

125

agt tac ctg aaa aag ggc tac ctg acc ctg tca gac agt ggg gac aag 552

Ser Tyr Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys

130

135

140

gtg gcc gtg gaa tgg gac aaa gac cat ggg gtc ctg gag tcc cac ctg 600

Val Ala Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu

145

150

155

gcg gag aag ggg aga ggc atg gag cta tcc gac ctg att gtt ttc aat 648

Ala Glu Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn

160

165

170

ggg aaa ctc tac tcc gtg gat gac cgg acg ggg gtc gtc tac cag atc 696

Gly Lys Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile

175

180

185

190

gaa ggc agc aaa gcc gtg ccc tgg gtg att ctg tcc gac ggc gac ggc 744

Glu Gly Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly

195

200

205

acc gtg gag aaa ggc ttc aag gcc gaa tgg ctg gca gtg cgg gag att 792

Thr Val Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile

210

215

220

gta agg aag cgg tgg cgg ctg gtg aag caa gtc tca cat gtc ggc gtt 840

Val Arg Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val

225

230

235

ctt ggc caa tgg ata caa aga taaagaaaat gttgcctttt tctaggaact 891

Leu Gly Gln Trp Ile Gln Arg

240

245

gtcagaaatc ctcatgcctt tcaagacttc tgtgaatgac ttgaattttt tattccctgc 951

ctagggctctg tgaacgaggc ctgtctcttc cctgggggttt ctttccatgg cctttatttc 1011

tcctcttcca gtgggagttt tgcaggetct tctctgtgga aacttcacga gcgttggtctg 1071

ggcctcggtc tcgctggagt gtactccagg gtgaaggcag agtgggattt gagaccagg 1131

tagtggagga agcgaaggaa gtgaacgctg aatgtgacgc atttctgaag agctcagctg 1191

tcaccgggca tagcctggaa gcccgaagtc tgttctgact ttgcctggct gtctccttga 1251

ccgcctcct agatcattgt ccttgatgtc caggctgggt catttaaat agagatgcaa 1311

tcaggaaggt tgggggactt gggactgtgg ctgaattgag accttgctga tgtattcatg 1371

tcagcacctg agtcacagcc caggtgcccg gaagcagcct cttcgcatag gcagtgattt 1431

gcgattactt taaagctcac cttttttctt cccctctctg ttcgctgctg tcagcataat 1491

gattgtgttc cttccctatg ggatccatct gttttgtaaa caataaagcg tctgaggag 1551

<210> 73

<211> 352

<212> PRT

<213> Homo sapiens

<400> 73

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly

1

5

10

15

Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys

20

25

30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly

35

40

45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro

50

55

60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn

65	70	75	80
Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu			
85	90	95	
Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp			
100	105	110	
Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu			
115	120	125	
Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro			
130	135	140	
Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His			
145	150	155	160
Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly			
165	170	175	
Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly			
180	185	190	
Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val			
195	200	205	
Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln			
210	215	220	

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp
 225 230 235 240

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe
 245 250 255

Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu
 260 265 270

Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser
 275 280 285

Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val
 290 295 300

Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val
 305 310 315 320

Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys
 325 330 335

Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser
 340 345 350

<210> 74

<211> 2401

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103)..(1158)

<400> 74

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tatccttggc gccacagtcg gccaccgggg ctgcccgcg tc atg gag agc gga 114

Met Glu Ser Gly

1

ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg 162

Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val

5

10

15

20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc 210

Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser

25

30

35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag 258

Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys

40

45

50

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata 306

Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile

55

60

65

gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg 354

Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val

70

75

80

gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag 402

Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys

85

90

95

100

atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc 450

Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile

105

110

115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag 498

Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu

120

125

130

gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg 546

Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val

135

140

145

gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag 594

Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln

150

155

160

tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa 642

Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys

165

170

175

180

ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca 690

Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr

185	190	195	
ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg			738
Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro			
200	205	210	
ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc			786
Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser			
215	220	225	
ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg			834
Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala			
230	235	240	
ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg			882
Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg			
245	250	255	260
aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag			930
Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln			
265	270	275	
gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct			978
Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro			
280	285	290	
gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc			1026
Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser			
295	300	305	

ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc 1074

Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr

310

315

320

gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga 1122

Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg

325

330

335

340

cag gcg atc acc cgg gtg ata ccc ccg tac aac agc taatagtttg 1168

Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser

345

350

gaagccgcac agcttgacct ggaagcaccc ctgccccctt ttcagggatt tttatctcga 1228

ggccttttga ggagcagtgg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288

tcgggtagaa actctccaga cccatgcctc caatggcagg atgctgcctt tcccacctga 1348

gaggggaccc tgtccatgtg cagcctcadc agagcctcac cctgggagga tgccgtggcg 1408

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caaagccagt gatcagcagc tcttctgttc ctgtgtcttc tgtttttttc tggatgaatcg 1528

ttgcttgctg tggacttggg ggaggactca gaggggagga aaggctgggc cccgagtaca 1588

acggatgcct tgggtgctgc ctccgaagag actctgccgc agcttttctt ctttttcctc 1648

atgccccggg aaacagtctt tcttcagaat tgtcaggctg ggcaggtcaa cttgtgttcc 1708
 tttccctca cctgcttgcc tccttaacgc ctgcacgtgt gtgtagagga caaaagaaag 1768
 tgaagtcagc acatccgctt ctgcccagat ggtcggggcc ccgggcaaca gattgaagag 1828
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 tcgcttctcc ttgtgttacc ccctcccagt attaccattt gcccctcacc tgcccttggt 2188
 gagcctttta gtgcaagaca gatggggctg ttttcccca cctctgagta gttggaggtc 2248
 acatacacag ctcttttttt attgcccttt tctgcctctg aatgttcac tctcgtcctc 2308
 ctttgtgcag gcgaggaagg ggtgccctca ggggccgaca ctagtgtgat gcagtgtcca 2368
 gtgtgaacag cagaaattaa acatgttgca acc 2401

<210> 75

<211> 352

<212> PRT

<213> Homo sapiens

<400> 75

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Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys
20 25 30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly
35 40 45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro
50 55 60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn
65 70 75 80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu
85 90 95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp
100 105 110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu
115 120 125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro

130

135

140

Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His
 145 150 155 160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly
 165 170 175

Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly
 180 185 190

Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val
 195 200 205

Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln
 210 215 220

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp
 225 230 235 240

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe
 245 250 255

Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu
 260 265 270

Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser
 275 280 285

Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val
290 295 300

Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val
305 310 315 320

Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys
325 330 335

Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser
340 345 350

<210> 76

<211> 2401

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103)..(1158)

<400> 76

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tatccttggc gccacagtcg gccaccgggg ctcgccgccg tc atg gag agc gga 114

Met Glu Ser Gly

1

ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg 162
 Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val
 5 10 15 20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc 210
 Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser
 25 30 35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag 258
 Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys
 40 45 50

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata 306
 Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile
 55 60 65

gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg 354
 Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val
 70 75 80

gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag 402
 Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys
 85 90 95 100

atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc 450
 Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile
 105 110 115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag 498

Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu	
120	125
130	
gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg 546	
Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val	
135	140
145	
gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag 594	
Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln	
150	155
160	
tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa 642	
Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys	
165	170
175	180
ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca 690	
Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr	
185	190
195	
ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg 738	
Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro	
200	205
210	
ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc 786	
Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser	
215	220
225	
ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg 834	
Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala	

230	235	240	
ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg			882
Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg			
245	250	255	260
aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag			930
Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln			
	265	270	275
gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct			978
Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro			
	280	285	290
gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc			1026
Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser			
	295	300	305
ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc			1074
Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr			
	310	315	320
gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga			1122
Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg			
325	330	335	340
cag gcg atc acc cgg gtg ata ccc ctg tac aac agc taatagtttg			1168
Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser			
	345	350	

gaagcgcac agcttgacct ggaagcacc cgtccccctt ttcagggatt tttatctcga 1228

ggcctttgga ggagcagtgg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288

tcgggtagaa actctccaga cccatgcctc caatggcagg atgctgcctt tcccacctga 1348

gaggggaccc tgtccatgtg cagcctcatc agagcctcac cctgggagga tgccgtggcg 1408

tctcctccca ggagccagat cagtgcgagt gtgactgaaa atgcctcatc acttaagcac 1468

caaagccagt gatcagcagc tcttctgttc ctgtgtcttc tggttttttc tggatgaatcg 1528

ttgcttgctg tggacttggt ggaggactca gaggggagga aaggctgggc cccgagtaca 1588

acggatgcct tgggtgctgc ctccgaagag actctgccgc agcttttctt ctttttcctc 1648

atgccccggg aaacagtctt tcttcagaat tgtcaggctg ggcaggtcaa cttgtgttcc 1708

tttccctca cctgcttgcc tccttaacgc ctgcacgtgt gtgtagagga caaaagaaag 1768

tgaagtcagc acatccgctt ctgccagat ggtcggggcc ccgggcaaca gattgaagag 1828

agatcatgtg aagggcagtt ggtcaggcag gcctcctggt ttcgccactg gccctgattt 1888

gaactcctgc cacttgggag agctcggggt ggccctggt tttccctcct ggagaatgag 1948

gcgcagaggc ctgcctcct gaaggacga gtgtggatgc cactggccta gtgtcctggc 2008

ctcacagctt ccttgcaagg ctgtcacaag gaaaagcagc cggctggcac cctgagcata 2068

tgccctcttg gggtccctc atccagcccg tcgcagcttt gacatcttgg tgtactcatg 2128

tcgcttctcc ttgtgttacc cctcctcagt attaccattt gccctcacc tgcccttggt 2188

gagcctttta gtgcaagaca gatggggctg ttttccccca cctctgagta gttggaggtc 2248

acatacacag ctcttttttt attgcccttt tctgcctctg aatgttcate tctcgtcctc 2308

ctttgtgcag gcgaggaagg ggtgccctca ggggccgaca ctagtgtgat gcagtgtcca 2368

gtgtgaacag cagaaattaa acatgttgca acc 2401

<210> 77

<211> 697

<212> PRT

<213> Homo sapiens

<400> 77

Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu Tyr Leu Ala

1 5 10 15

Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met His Ser Ser

20 25 30

Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu Val Ala Ile

35 40 45

Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn Ser Leu Ile
50 55 60

Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile Ala Ser Ile
65 70 75 80

Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser Leu Ser Asn
85 90 95

Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser
100 105 110

Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu
115 120 125

Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg Ile Ser
130 135 140

Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu Phe Leu
145 150 155 160

Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val Glu Lys
165 170 175

Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu Ile Ile
180 185 190

Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val Ile Phe

195	200	205
Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile		
210	215	220
Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp		
225	230	235 240
Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro Phe Leu		
245	250	255
Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala Gly Met		
260	265	270
Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr		
275	280	285
His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe		
290	295	300
Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly Phe His		
305	310	315 320
Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg Thr Asp		
325	330	335
Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg His Phe		
340	345	350

Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala Thr Ala
355 360 365

Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser
370 375 380

Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly Leu Phe
385 390 395 400

His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile
405 410 415

Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu
420 425 430

Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly Met Leu
435 440 445

Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr Tyr Gly
450 455 460

Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His Ser Lys
465 470 475 480

Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg His Asp
485 490 495

Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly Glu Trp
500 505 510

Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp

515

520

525

Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile Val Leu

530

535

540

Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys Ile Asn

545

550

555

560

Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr Val Asp

565

570

575

Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp

580

585

590

Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys

595

600

605

Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp Ser Asp

610

615

620

Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His Trp Met

625

630

635

640

Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala Asn Trp

645

650

655

Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys

660

665

670

Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu Asp Thr

675

680

685

Gly Gln Gly Phe Lys Leu Val Lys Ser

690

695

<210> 78

<211> 3008

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (372)..(2462)

<400> 78

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ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgtctt cctccttttt 180

ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300

ttggatatac tggatgaaat acaagcgggtt aatttttgta acgtgaggga aaagcccaca 360

ttgctgggta c atg tgt aaa tca ctg cgt tat tgc ttt agt cat tgt ctc 410

Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu

1

5

10

tat tta gca atg aca aga ctg gaa gaa gta aat aga gaa gtg aac atg 458

Tyr Leu Ala Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met

15

20

25

cat tct tca gtg cgg tat ctt ggc tat tta gcc aga atc aat tta ttg 506

His Ser Ser Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu

30

35

40

45

gtt gct ata tgc tta ggt cta tac gta aga tgg gaa aaa aca gca aat 554

Val Ala Ile Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn

50

55

60

tcc tta att ttg gta att ttt att ctt ggt ctt ttt gtt ctt gga atc 602

Ser Leu Ile Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile

65

70

75

gcc agc ata ctc tat tac tat ttt tca atg gaa gca gca agt tta agt 650

Ala Ser Ile Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser

80

85

90

ctc tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt 698

Leu Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu

95

100

105

gat aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat 746
 Asp Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr
 110 115 120 125

ttg ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag 794
 Leu Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu
 130 135 140

aga att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt 842
 Arg Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val
 145 150 155

gaa ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg 890
 Glu Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu
 160 165 170

gtg gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg 938
 Val Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met
 175 180 185

ctg att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta 986
 Leu Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu
 190 195 200 205

gtt att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa 1034
 Val Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys
 210 215 220

aat ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct 1082
 Asn Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro

225

230

235

ttc ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa 1130
 Phe Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys

240

245

250

ccc ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt 1178
 Pro Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe

255

260

265

gct gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt 1226
 Ala Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu

270

275

280

285

aga gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt 1274
 Arg Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe

290

295

300

gga att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg 1322
 Gly Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp

305

310

315

gga ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac 1370
 Gly Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His

320

325

330

agg aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg 1418

Arg Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met
 335 340 345

cgc cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt 1466
 Arg His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu
 350 355 360 365

gca aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att 1514
 Ala Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile
 370 375 380

ttc ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat 1562
 Phe Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His
 385 390 395

ggg ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga 1610
 Gly Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly
 400 405 410

tat gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca 1658
 Tyr Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro
 415 420 425

aca ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act 1706
 Thr Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr
 430 435 440 445

ggc atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag 1754
 Gly Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu

450	455	460	
acc tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg			1802
Thr Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu			
465	470	475	
cat tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc			1850
His Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro			
480	485	490	
aga cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca			1898
Arg His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr			
495	500	505	
gga gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt			1946
Gly Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu			
510	515	520	525
ata gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att			1994
Ile Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile			
530	535	540	
atc gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg			2042
Ile Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg			
545	550	555	
aaa att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa			2090
Lys Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys			
560	565	570	

aca gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca 2138

Thr Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr

575

580

585

aaa gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg 2186

Lys Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp

590

595

600

605

act gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg 2234

Thr Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg

610

615

620

tgg agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag 2282

Trp Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys

625

630

635

cac tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg 2330

His Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu

640

645

650

gca aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt 2378

Ala Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys

655

660

665

ttt agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg 2426

Phe Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val

670

675

680

685

ctg gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac 2472

Leu Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser

690

695

cccaaagcgg gatattaata agcactcata ctaccaatta tcactaactt gccatttttt 2532

gtatgctgta tttttatttg tggaaaatac cttgctactt ctgtagctgc tctcactttg 2592

tcttttctta agtaattatg gtatatataa ggcgttggga aaaaacattt tataatgaaa 2652

gtatgtaggg agtcaaatgc ttactgtaaa tgcataagag acgttaaaaa taacactgca 2712

ctttcaggaa tgtttgctta tggtcctgat tagaaagaaa cagttgtcta tgctctgcaa 2772

tggatcaatga tgaattacta atgccttatt ttctagggcat ataataatag tttagagaat 2832

gtagaccaga taaatttggt tactgtttta agaaaactac cagtttactt acagaagatt 2892

cttttttcca aacagtaggt ttcatccaag accatttgaa gaactgcaaa ctctttctct 2952

tagaaaagaa agagggcagc ctaaaataaa cgcaaaatgt gcttatactc catcac 3008

<210> 79

<211> 611

<212> PRT

<213> Homo sapiens

<400> 79

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Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser Ser Phe Lys Asn Asp Val
20 25 30

Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu Thr Ser Ile Val Leu Arg
35 40 45

Ile Leu Cys Ser Leu Val Glu Arg Ile Ser Gly Tyr Val Arg His Arg
50 55 60

Pro Thr Leu Leu Thr Thr Val Glu Phe Leu Glu Leu Val Gly Phe Ala
65 70 75 80

Ile Ala Ser Thr Thr Met Leu Val Glu Lys Ser Leu Ser Val Ile Leu
85 90 95

Leu Val Val Ala Leu Ala Met Leu Ile Ile Asp Leu Arg Met Lys Ser
100 105 110

Phe Leu Ala Ile Pro Asn Leu Val Ile Phe Ala Val Leu Leu Phe Phe
115 120 125

Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile Ala Phe Ala Cys Phe Phe
130 135 140

Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp Ile Tyr Phe Ser Gly Leu
145 150 155 160

Ser Val Thr Glu Arg Trp Lys Pro Phe Leu Tyr Arg Gly Arg Ile Cys
165 170 175

Arg Arg Leu Ser Val Val Phe Ala Gly Met Ile Glu Leu Thr Phe Phe
180 185 190

Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr His Leu Trp Tyr Phe Val
195 200 205

Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe Trp Met Ile Cys His Ile
210 215 220

Ile Phe Leu Leu Thr Leu Trp Gly Phe His Thr Lys Leu Asn Asp Cys
225 230 235 240

His Lys Val Tyr Phe Thr His Arg Thr Asp Tyr Asn Ser Leu Asp Arg
245 250 255

Ile Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile Ser Glu Gln
260 265 270

Leu Val Phe Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly Ala Val Ser
275 280 285

Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu Ile Val Leu
290 295 300

Pro Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu Gly Asn Cys
273/754

305	310	315	320
Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro Thr Asn Phe			
325	330	335	
Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu His Val Gln			
340	345	350	
Glu Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile Gln Arg Phe			
355	360	365	
Phe Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr Ser Thr Ser			
370	375	380	
Gly Leu Ser Phe Asp Thr Leu His Ser Lys Leu Lys Ala Phe Leu Glu			
385	390	395	400
Leu Arg Thr Val Asp Gly Pro Arg His Asp Thr Tyr Ile Leu Tyr Tyr			
405	410	415	
Ser Gly His Thr His Gly Thr Gly Glu Trp Ala Leu Ala Gly Gly Asp			
420	425	430	
Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp Trp Arg Glu Lys Asn Gly			
435	440	445	
Ser Phe Cys Ser Arg Leu Ile Ile Val Leu Asp Ser Glu Asn Ser Thr			
450	455	460	

Pro Trp Val Lys Glu Val Arg Lys Ile Asn Asp Gln Tyr Ile Ala Val
465 470 475 480

Gln Gly Ala Glu Leu Ile Lys Thr Val Asp Ile Glu Glu Ala Asp Pro
485 490 495

Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp Val Glu Tyr Asn Cys Asn
500 505 510

Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys Gly Arg Thr Val Lys Ala
515 520 525

Val Tyr Gly Val Ser Lys Arg Trp Ser Asp Tyr Thr Leu His Leu Pro
530 535 540

Thr Gly Ser Asp Val Ala Lys His Trp Met Leu His Phe Pro Arg Ile
545 550 555 560

Thr Tyr Pro Leu Val His Leu Ala Asn Trp Leu Cys Gly Leu Asn Leu
565 570 575

Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys Leu Lys Arg Leu Lys Met
580 585 590

Ser Trp Phe Leu Pro Thr Val Leu Asp Thr Gly Gln Gly Phe Lys Leu
595 600 605

Val Lys Ser
610

<210> 80

<211> 3007

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (629)..(2461)

<400> 80

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aaagtttacg ccgacactgg cctgtattag cgcgtatggc ctcgggccct cgttccccaa 120

ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180

ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300

ttggatatac tggatgaaat acaagcggtt aatttttgta acgtgaggga aaagcccaca 360

ttgctggtta catgtgtaaa tcaactgcgtt attgcttttag tcattgtctc tatttagcaa 420

tgacaagact ggaagaagta aatagagaag tgaacatgca ttcttcagtg cggatatcttg 480

ctattttagcc agaatcaatt tattggttgc tatatgetta ggtctatacg taagatggga 540

aaaaacagca aattccttaa ttttgtaat ttttattctt ggtctttttg ttcttggaat 600

cgccagcata ctctattact atttttca atg gaa gca gca agt tta agt ctc 652

Met Glu Ala Ala Ser Leu Ser Leu

1

5

tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt gat 700

Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp

10

15

20

aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat ttg 748

Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu

25

30

35

40

ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag aga 796

Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg

45

50

55

att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt gaa 844

Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu

60

65

70

ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg gtg 892

Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val

75

80

85

gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg ctg 940

Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu

90	95	100	
att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta gtt			988
Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val			
105	110	115	120
att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa aat			1036
Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn			
	125	130	135
ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct ttc			1084
Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe			
	140	145	150
ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa ccc			1132
Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro			
	155	160	165
ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt gct			1180
Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala			
170	175	180	
gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt aga			1228
Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg			
185	190	195	200
gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt gga			1276
Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly			
	205	210	215

att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg gga 1324

Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly

220

225

230

ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac agg 1372

Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg

235

240

245

aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg cgc 1420

Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg

250

255

260

cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt gca 1468

His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala

265

270

275

280

aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att ttc 1516

Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe

285

290

295

ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat ggg 1564

Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly

300

305

310

ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga tat 1612

Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr

315

320

325

gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca aca 1660
 Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr
 330 335 340

ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act ggc 1708
 Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly
 345 350 355 360

atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag acc 1756
 Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr
 365 370 375

tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg cat 1804
 Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His
 380 385 390

tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc aga 1852
 Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg
 395 400 405

cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca gga 1900
 His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly
 410 415 420

gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt ata 1948
 Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile
 425 430 435 440

gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att atc 1996

Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile

445

450

455

gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg aaa 2044

Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys

460

465

470

att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa aca 2092

Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr

475

480

485

gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca aaa 2140

Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys

490

495

500

gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg act 2188

Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr

505

510

515

520

gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg tgg 2236

Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp

525

530

535

agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag cac 2284

Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His

540

545

550

tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg gca 2332

Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala

555

560

565

aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt ttt 2380

Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe

570

575

580

agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg ctg 2428

Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu

585

590

595

600

gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac cccaaagcgg 2481

Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser

605

610

gatattaata agcactcata ctaccaatta tcactaactt gccatttttt gtatgctgta 2541

tttttatattg tggaaaatac ctgtctactt ctgtagctgc tctcactttg tcttttctta 2601

agtaattatg gtatatataa ggcgttggga aaaaacattt tataatgaaa gtatgtaggg 2661

agtcaaatgc ttactgtaaa tgcataagag acgttaaaaa taacactgca ctttcaggaa 2721

tgtttgctta tggtcctgat tagaaagaaa cagttgtcta tgctctgcaa tggatcaatga 2781

tgaattacta atgccttatt ttctaggcat ataataatag tttagagaat gtagaccaga 2841

taaatttggt tactgtttta agaaaactac cagtttactt acagaagatt cttttttcca 2901

aacagtaggt ttcatccaag accatttgaa gaactgcaaa ctctttctct tagaaaagaa 2961

agagggcagc ctaaaataaa cgcaaaattt gcttatactc catcac

3007

<210> 81

<211> 184

<212> PRT

<213> Homo sapiens

<400> 81

Met Thr Ser Phe Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu

1 5 10 15

Gln Met Thr Val Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln

20 25 30

Ser Ile Ser Phe Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys

35 40 45

Phe Gly Arg Asn Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln

50 55 60

Val Ser Arg Val Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser

65 70 75 80

Ser Val Leu Ser Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu

85 90 95

Ile Val Asp Ser Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro

100	105	110
Tyr Arg Cys Met Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys		
115	120	125
Glu Asp Gly Glu Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser		
130	135	140
Pro Arg Ser Leu Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile		
145	150	155
Pro Glu Tyr Gly Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro		
165	170	175
Thr Glu Met Asp Glu Asn Glu Ser		
180		

<210> 82

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (285).. (836)

<400> 82

tttttacaaa ggccccgggc gcgagaggac gtgctctgcc agccagtggg aaggcaggcc 60

gcgcgcgcgg gagcgcggga ggatcggcgg ctgcggtca ctgggccctg gctcggttcc 120

ccgcaccccc gggtcacac ttaccgcgc ggaggagcag cggccgggtg tccaccccca 180

tcctgcgcc agtctctctg attcccctcg ctctgagccg ggagagccga acagctgaag 240

agagttcact gactccccag cccaggtgg gccttgtgca catc atg acc agt ttt 296

Met Thr Ser Phe

1

gaa gat gct gac aca gaa gag aca gta act tgt ctc cag atg acg gtt 344

Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu Gln Met Thr Val

5

10

15

20

tac cat cct ggc cag ttg cag tgt gga ata ttt cag tca ata agt ttt 392

Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln Ser Ile Ser Phe

25

30

35

aac aga gag aaa ctc cct tcc agc gaa gtg gtg aaa ttt ggc cga aat 440

Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys Phe Gly Arg Asn

40

45

50

tcc aac atc tgt cat tat act ttt cag gac aaa cag gtt tcc cga gtt 488

Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln Val Ser Arg Val

55

60

65

cag ttt tct ctg cag ctg ttt aaa aaa ttc aac agc tca gtt ctc tcc 536

Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser Ser Val Leu Ser

70	75	80	
ttt gaa ata aaa aat atg agt aaa aag acc aat ctg atc gtg gac agc	584		
Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu Ile Val Asp Ser			
85	90	95	100
aga gag ctg ggc tac cta aat aaa atg gac ctg cca tac agg tgc atg	632		
Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro Tyr Arg Cys Met			
105	110	115	
gtc aga ttc gga gag tat cag ttt ctg atg gag aag gaa gat ggc gag	680		
Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys Glu Asp Gly Glu			
120	125	130	
tca ttg gaa ttt ttt gag act caa ttt att tta tct cca aga tca ctc	728		
Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser Pro Arg Ser Leu			
135	140	145	
ttg caa gaa aac aac tgg cca cca cac agg ccc ata ccg gag tat ggc	776		
Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile Pro Glu Tyr Gly			
150	155	160	
act tat tcg ctc tgc tcc tcc caa agc agt tct ccg aca gaa atg gat	824		
Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro Thr Glu Met Asp			
165	170	175	180
gaa aat gag tca tgaacacaga aagtctaaga ggagaaatat gatggatgaa	876		
Glu Asn Glu Ser			

gagctctgta gatgctgtat agacactaaa taagagttga ttagggtagt atattatagt 936
catctgttat gctgtgaaat ttggaattca gtattatcat tttgaagtct gtaaattgtg 996
ttagtcatta acttagtcac ctgttgtatt ctggatctac acaaaattat tttactgct 1056
cttattaatc tgtgaggatt aatatacaaa aagtatcctt tgagatgaag tegtgttctc 1116
aaaataaggt tatattatct tcttttctg ctgtatttc atcttgtgtt ttgctttgtt 1176
tttgaagga accatctctt ggtttggtca catcagttca caacagccat ttgttttcaa 1236
ggtcaaggct ccaggcaggt tgttactggt gtttcagcc tgcagtact tgcagtactg 1296
gaatagggtc taggctagtg tctgcgcgtc actgtgggtt tagcatggga ggacttatct 1356
gagaaatact accttacttt tctatgattt ctttttacag agttatagtg tgtttactcc 1416
taagatgaca gttctctttg tctatattca gcactaaga caaatattta aacattttaa 1476
agaaccactg tgttaagttt aggattattt acttacaaa ttagaagttt gacttttatg 1536
tggtatacac aatcttaaaa ttccacgaat tcacctttt aatagtatcc atgtacataa 1596
taaaatcaaa gtttaattag c 1617

<210> 83

<211> 392

<212> PRT

<213> Homo sapiens

<400> 83

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
1 5 10 15

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
20 25 30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
35 40 45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
50 55 60

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
65 70 75 80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
85 90 95

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
100 105 110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
115 120 125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser

130	135	140	
Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg			
145	150	155	160
Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln			
	165	170	175
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser			
	180	185	190
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser			
	195	200	205
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met			
	210	215	220
Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr			
	225	230	235
			240
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser			
	245	250	255
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu			
	260	265	270
Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr			
	275	280	285

Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu
290 295 300

Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly
305 310 315 320

Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala
325 330 335

Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val
340 345 350

Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg
355 360 365

Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro
370 375 380

Val Glu Ser Pro Val Gln Lys Val
385 390

<210> 84

<211> 1898

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119).. (1294)

<400> 84

acttccgctg gccgctggct cgctggccgc tcctggaggc ggcggcggga gcgcaggggg 60

cgcgcgggccc ggggactcgc attccccggt tccccctcca ccccacggcg cctggacc 118

atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc 166

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1 5 10 15

cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc 214

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

20 25 30

cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc 262

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser

35 40 45

ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac 310

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn

50 55 60

tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt 358

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys

65 70 75 80

gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc 406

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro

85

90

95

cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg 454

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu

100

105

110

ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg 502

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val

115

120

125

ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca 550

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser

130

135

140

ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg cta atg aac cga 598

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg

145

150

155

160

gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag 646

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln

165

170

175

ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc 694

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser

180

185

190

aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc 742

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser

195

200

205

ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg 790

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met

210

215

220

ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac 838

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr

225

230

235

240

ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc 886

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser

245

250

255

agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc 934

Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu

260

265

270

ttc aca gtg ggc tca ctg cta gaa cag ggg gcc cta ctg gag gga acc 982

Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr

275

280

285

cgc ttc atg ggg cga cac agt gag ttt gct gcc cat gcc ctg cta ctc 1030

Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu

290

295

300

tcc atc tgc tcc gca tgt ggc cag ctc ttc atc ttt tac acc att ggg 1078

Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly

305

310

315

320

cag ttt ggg gct gcc gtc ttc acc atc atc atg acc ctc cgc cag gcc 1126

Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala

325

330

335

ttt gcc atc ctt ctt tcc tgc ctt ctc tat ggc cac act gtc act gtg 1174

Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val

340

345

350

gtg gga ggg ctg ggg gtg gct gtg gtc ttt gct gcc ctc ctg ctc aga 1222

Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg

355

360

365

gtc tac gcg cgg ggc cgt cta aag caa cgg gga aag aag gct gtg cct 1270

Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro

370

375

380

gtt gag tct cct gtg cag aag gtt tgagggtgga aagggcctga ggggtgaagt 1324

Val Glu Ser Pro Val Gln Lys Val

385

390

gaaataggac cctcccacca tccccttctg ctgtaacctc tgagggagct ggctgaaagg 1384

gcaaaatgca ggtgttttct cagtatcaca gaccagctct gcagcagggg attggggagc 1444

ccaggaggca gccttccctt ttgccttaag tcacccatct tccagtaage agttttattct 1504

gagccccggg ggtagacagt cctcagttag gggttttggg gagttttggg tcaagagagc 1564

ataggtaggt tccacagtta ctcttccac aagttccctt aagtcttgcc ctagctgtgc 1624

tctgccacct tccagactca ctccccctctg caaataacctg catttcttac cctgggtgaga 1684

aaagcacaag cgggtgtaggc tccaatgctg ctttcccagg aggggtgaaga tgggtgctgtg 1744

ctgaggaaag gggatgcaga gccctgcccga gcaccaccac ctcctatgct cctggatccc 1804

taggctctgt tccatgagcc tgttgcaggt tttggtactt tagaaatgta actttttgct 1864

cttataattt tattttatta aattaaatta ctgc 1898

<210> 85

<211> 432

<212> PRT

<213> Homo sapiens

<400> 85

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1 5 10 15

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

20 25 30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser

35 40 45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn

50 55 60

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
65 70 75 80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
85 90 95

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
100 105 110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
115 120 125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
130 135 140

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145 150 155 160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
165 170 175

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
180 185 190

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
195 200 205

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met

210	215	220	
Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr			
225	230	235	240
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser			
	245	250	255
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu			
	260	265	270
Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp			
	275	280	285
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe			
	290	295	300
Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu			
305	310	315	320
Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu			
	325	330	335
Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln			
	340	345	350
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr			
	355	360	365

Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu
370 375 380

Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
385 390 395 400

Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys
405 410 415

Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val
420 425 430

<210> 86

<211> 2018

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119)..(1414)

<400> 86

acttccgctg gccgctggct cgctggccgc tcctggaggc ggcggcggga ggcaggggg 60

cgcgcgggccc ggggactcgc attccccggt tccccctcca cccacgcgg cctggacc 118

atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc 166

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1	5	10	15	
cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc				214
Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr				
	20	25	30	
cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc				262
Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser				
	35	40	45	
ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac				310
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn				
	50	55	60	
tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt				358
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys				
	65	70	75	80
gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc				406
Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro				
	85	90	95	
cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg				454
Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu				
	100	105	110	
ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg				502
Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val				
	115	120	125	

ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca 550
 Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser

130

135

140

ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg cta atg aac cga 598
 Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg

145

150

155

160

gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag 646
 Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln

165

170

175

ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc 694
 Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser

180

185

190

aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc 742
 Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser

195

200

205

ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg 790
 Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met

210

215

220

ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac 838
 Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr

225

230

235

240

ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc	886
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser	
245 250 255	
agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc	934
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu	
260 265 270	
atc tta ctg gca ggt tat att gct ttt gac agc ttc acc tca aac tgg	982
Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp	
275 280 285	
cag gat gcc ctg ttt gcc tat aag atg tca tgc gtg cag atg atg ttt	1030
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe	
290 295 300	
ggg gtc aat ttc ttc tcc tgc ctc ttc aca gtg ggc tca ctg cta gaa	1078
Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu	
305 310 315 320	
cag ggg gcc cta ctg gag gga acc cgc ttc atg ggg cga cac agt gag	1126
Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu	
325 330 335	
ttt gct gcc cat gcc ctg cta ctc tcc atc tgc tcc gca tgt ggc cag	1174
Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln	
340 345 350	
ctc ttc atc ttt tac acc att ggg cag ttt ggg gct gcc gtc ttc acc	1222

Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr
355 360 365

atc atc atg acc ctc cgc cag gcc ttt gcc atc ctt ctt tcc tgc ctt 1270
Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu
370 375 380

ctc tat ggc cac act gtc act gtg gtg gga ggg ctg ggg gtg gct gtg 1318
Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
385 390 395 400

gtc ttt gct gcc ctc ctg ctc aga gtc tac gcg cgg ggc cgt cta aag 1366
Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys
405 410 415

caa cgg gga aag aag gct gtg cct gtt gag tct cct gtg cag aag gtt 1414
Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val
420 425 430

tgagggtgga aagggcctga ggggtgaagt gaaataggac cctcccacca tccccttctg 1474

ctgtaacctc tgaggagct ggctgaaagg gcaaaatgca ggtgttttct cagtatcaca 1534

gaccagctct gcagcagggg attggggagc ccaggaggca gccttccctt ttgccttaag 1594

tcacccatct tccagtaagc agttttattct gagccccggg ggtagacagt cctcagttag 1654

gggttttggg gagtttgggg tcaagagagc ataggttagt tccacagtta ctcttccac 1714

aagttccctt aagtcttgcc ctagctgtgc tctgccacct tccagactca ctcccctctg 1774

caaataacctg catttcttac cctggtgaga aaagcacaag cgggtgtaggc tccaatgctg 1834

ctttcccagg aggggtgaaga tgggtgctgtg ctgaggaaag gggatgcaga gccctgceca 1894

gcaccaccac ctccatgct cctggatccc taggctctgt tccatgagcc tgttgcaggt 1954

tttggtaactt tagaaatgta actttttgct cttataattt tattttatta aattaaatta 2014

ctgc 2018

<210> 87

<211> 235

<212> PRT

<213> Homo sapiens

<400> 87

Met Gly Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser

1 5 10 15

Trp Gly Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser

20 25 30

Asp Ser Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His

35 40 45

Ser Asn Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser

50		55		60
Val Glu Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys				
65		70		75
				80
Phe Val Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val				
	85		90	95
Gln Asn Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe				
	100		105	110
Ala Glu Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala				
	115		120	125
Val Asn Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu				
	130		135	140
Arg Asp Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser				
145		150		155
				160
Val Asn Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu				
	165		170	175
Asn Asn Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile				
	180		185	190
Asn Ala Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg				
	195		200	205

Ile Phe Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu
 210 215 220

Thr Arg Asn Met Val Gln Arg Gln Phe Ile Ala
 225 230 235

<210> 88

<211> 2717

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (111).. (815)

<400> 88

aaaaggaaga cagaaaagcc gcgggctgac tgtggtggcg ctgcctgca gattgaaaag 60

aaatgctgag aaatacataa agttttcctc ttctgccttg gatatttata atg ggt 116

Met Gly

1

atc ggg aag tct aaa ata aat tcc tgc cct ctt tct ctc tct tgg ggt 164

Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser Trp Gly

5

10

15

aaa agg cac agt gtg gat aca agt cca gga tat cat gag tca gat tcc 212

Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser Asp Ser

20	25	30	
aag aag tct gaa gat cta tcc ttg tgt aat gtt gct gag cac agc aat	260		
Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His Ser Asn			
35	40	45	50
aca aca gag ggg cca aca gga aag cag gag gga gct cag agc gtg gaa	308		
Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser Val Glu			
55	60	65	
gag atg ttt gaa gaa gaa gct gaa gaa gag gtg ttc ctc aaa ttt gtg	356		
Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys Phe Val			
70	75	80	
ata ttg cat gca gaa gat gac aca gat gaa gcc ctc aga gtc cag aat	404		
Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val Gln Asn			
85	90	95	
ctg cta caa gat gac ttt ggt atc aaa ccc gga ata atc ttt gct gag	452		
Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe Ala Glu			
100	105	110	
atg cca tgt ggc aga cag cat tta cag aat tta gat gat gct gta aat	500		
Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala Val Asn			
115	120	125	130
ggg tct gca tgg aca atc tta tta ctg act gaa aac ttt tta aga gat	548		
Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu Arg Asp			
135	140	145	

act tgg tgt aat ttc cag ttc tat acg tcc cta atg aac tcc gtt aac 596

Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser Val Asn

150

155

160

agg cag cat aaa tac aac tct gtt ata ccc atg cgg ccc ctg aac aat 644

Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu Asn Asn

165

170

175

ccc ctt ccc cga gaa agg act ccc ttt gcc ctc caa acc atc aat gcc 692

Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile Asn Ala

180

185

190

tta gag gaa gaa agt cgt gga ttt cct aca caa gta gaa aga att ttt 740

Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg Ile Phe

195

200

205

210

cag gag tct gtg tat aag aca caa caa act ata tgg aaa gag aca aga 788

Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu Thr Arg

215

220

225

aat atg gta caa aga caa ttt att gcc tgagatgaaa catataacat 835

Asn Met Val Gln Arg Gln Phe Ile Ala

230

235

gtggctggct cttgttttgt aaaccaaagtg attaatcttc acttgagaaa gcagtttcta 895

ggaaatgttt aaataaaaga gagtccttcac cttaaagaaa cctatggagc acaagaaaga 955

taaatttctg caggacagcc tataaaattg tggtagcttt tgatgtttca gtaaacttga 1015

cattgtcaga gtttcaagga cttttctttc acaattttcc tagttcatgg atatgaaaaa 1075

ggaattctca atccatattc ctgtattga acctgaaca aaaacttgta tgacagacat 1135

ttttaaaaat gtgacaacac ttttattctc tgaattttga tctcaaagga cacagaaaaa 1195

aaatggcccc aggagatctg atcacacttc ctctgagge acctctcatg gatgttgcaa 1255

taagcattcg ggtactatca ccagaaata tgaattgcca gaatagaaca tttagcatgt 1315

taagcgttga tgcatataaa atcagaaata gatgtgagaa tgggtggaact ttttaaaga 1375

accagtcaa atgtattttc tgctgaaatc tgcatatttg gaggcatttc ccaccaccga 1435

ttcacagccc atttgatagt gtggtagtta gggacttcgt ggagtgggtg tcagacgtcc 1495

cctggggctt aaatctcttc atattagtca tcatttgtaa ctatggcttt atttgagag 1555

cttctaaaag gcgtataact gtgtgagtgg ccagatattc actttttaga tcaaaaacct 1615

ctcttatgga agctttaaaa gtttcctgca cacacaattc tcttctcagg aagtatttct 1675

catttaggtc ttcaaagtag cctgactgtg tgcatgtgtg tgtgtgatag gttatttata 1735

aagactttgg atagaaggag atgtatttta ttacctcta ttctagagcc ccatgctcct 1795

aacaagccag agaggcccca aacaggattg tttctttcct ccacagccct tctgcccac 1855

tgagattgag ggagcatcgt ccacttgaga tcagggatgg ggtggagaat gggtcatgtc 1915

atgtaatgag aaaagccctc ttcgggatca tgagacttgg ttctagtcca atttctgcca 1975

ctgaggatga atgtaactgt gggcaaaacta tttaccctcc tttatctgtg aaatgaaagg 2035

gttgaattga tggatctcta aaggcttttg tcctctatga ggatgtgaaa aactagggac 2095

cacaaaaggg aacaagcaaa aaagtttggg ttcgataaag tgatatgtaa tagttgcaga 2155

aggttttata tatgcttata atgaaaagat attttttgta tattgacagc ataatttatt 2215

tttaatgctg tcattacact taaagtcaca ggaaaaaaat atacatgctt actcaggctt 2275

tcttaaaaaat aaatttttat agagatcctt gagtaaagac attttgctta atttcttttt 2335

tcttatcccc cacttgata tccccacca gtaccgggat ctgcacacat ctttttgcag 2395

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tcctattctg ttagtactta ttagaggagg agatggtttt cattgcatag tgacattttc 2515

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agtattcatt tttttgcat aatgcttcct gtaaagccaa ttttatatac taataaaaca 2635

tgaactgccc actcttcatg cctgccaaac ttggggcaat tgatgctaaa tggatatttt 2695

aaaataaatg tttttattct tt

2717

<210> 89

<211> 245

<212> PRT

<213> Homo sapiens

<400> 89

Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys

1 5 10 15

Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly

20 25 30

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn

35 40 45

Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu

50 55 60

Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe

65 70 75 80

Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe

85 90 95

Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe

100 105 110

310/754

Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys
115 120 125

Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val
130 135 140

Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg
145 150 155 160

Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser
165 170 175

Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val
180 185 190

Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu
195 200 205

Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu
210 215 220

Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn
225 230 235 240

Gln Tyr Glu Ile Val
245

<210> 90

<211> 1793

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (60)..(794)

<400> 90

gcgtctcgct ctctgtgttc caatcgcccg gtgcggtggt gcagggtctc gggctagtc 59

atg gcg tcc ccg tct cgg aga ctg cag act aaa cca gtc att act tgt 107

Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys

1

5

10

15

ttc aag agc gtt ctg cta atc tac act ttt att ttc tgg atc act ggc 155

Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly

20

25

30

gtt atc ctt ctt gca gtt ggc att tgg ggc aag gtg agc ctg gag aat 203

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn

35

40

45

tac ttt tct ctt tta aat gag aag gcc acc aat gtc ccc ttc gtg ctc 251

Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu

50

55

60

att gct act ggt acc gtc att att ctt ttg ggc acc ttt ggt tgt ttt 299

Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe
65 70 75 80

gct acc tgc cga gct tct gca tgg atg cta aaa ctg tat gca atg ttt 347
Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe
85 90 95

ctg act ctc gtt ttt ttg gtc gaa ctg gtc gct gcc atc gta gga ttt 395
Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe
100 105 110

gtt ttc aga cat gag att aag aac agc ttt aag aat aat tat gag aag 443
Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys
115 120 125

gct ttg aag cag tat aac tct aca gga gat tat aga agc cat gca gta 491
Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val
130 135 140

gac aag atc caa aat acg ttg cat tgt tgt ggt gtc acc gat tat aga 539
Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg
145 150 155 160

gat tgg aca gat act aat tat tac tca gaa aaa gga ttt cct aag agt 587
Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser
165 170 175

tgc tgt aaa ctt gaa gat tgt act cca cag aga gat gca gac aaa gta 635
Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val

180

185

190

aac aat gaa ggt tgt ttt ata aag gtg atg acc att ata gag tca gaa 683

Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu

195

200

205

atg gga gtc gtt gca gga att tcc ttt gga gtt gct tgc ttc caa ctg 731

Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu

210

215

220

att gga atc ttt ctc gcc tac tgc ctc tct cgt gcc ata aca aat aac 779

Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn

225

230

235

240

cag tat gag ata gtg taacccaatg tatctgtggg cctattcctc tctaccttta 834

Gln Tyr Glu Ile Val

245

aggacattta ggggtcccccc tgtgaattag aaagttgctt ggctggagaa ctgacaacac 894

tacttactga tagaccaaaa aactacacca gtaggttgat tcaatcaaga tgtatgtaga 954

cctaaaacta caccaatagg ctgattcaat caagatccgt gctcgcagtg ggctgattca 1014

atcaagatgt atgtttgcta tggttctaagt ccacattcta tccattcat gttagatcgt 1074

tgaaaccctg tatccctctg aaacactgga agagctagta aattgtaaat gaagtaatac 1134

tgtgttcctc ttgactgtta tttttcttag tagggggcct ttggaaggca ctgtgaattt 1194

gctatTTTtga tgtagtgTta caagatggaa aattgattcc tctgactttg ctattgatgt 1254

agtgtgatag aaaattcacc cctctgaact ggctccttcc cagtcaaggt tatctggttt 1314

gattgtataa tttgcaccaa gaagttaaaa tgTTTTatga ctctctgttc tgctgacagg 1374

cagagagtca cattgtgtaa tTTaatttca gtcagtcaat agatggcatc cctcatcagg 1434

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ttcgtttgtg cctttgatta ataagtataa ctcttataca ataaatactg ctttctct 1793

<210> 91

<211> 180

<212> PRT

<213> Homo sapiens

<400> 91

Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly

1	5	10	15
Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu			
20	25	30	
Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala			
35	40	45	
Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg			
50	55	60	
Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly			
65	70	75	80
Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met			
85	90	95	
Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys			
100	105	110	
Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln			
115	120	125	
Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu			
130	135	140	
Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser			
145	150	155	160

Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
165 170 175

Ala Leu Leu Gln
180

<210> 92

<211> 970

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26)..(565)

<400> 92

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Met Ala Ser Thr Ser Tyr Asp Tyr Cys
1 5

aga gtg ccc atg gaa gac ggg gat aag cgc tgt aag ctt ctg ctg ggg 100
Arg Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly
10 15 20 25

ata gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg 148
Ile Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu
30 35 40

att atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt 196
 Ile Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu

45

50

55

cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag 244
 Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu

60

65

70

ctg acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gct gcc 292
 Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala

75

80

85

acc tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag 340
 Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu

90

95

100

105

aag gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act 388
 Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr

110

115

120

aca tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg 436
 Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu

125

130

135

aga aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac 484
 Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr

140

145

150

tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg 532

Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu

155

160

165

att gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctggc 585

Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln

170

175

180

acatcttgga aggtccgtcc tgctcggctt ttcgcttgaa cattcccttg atctcatcag 645

ttctgagcgg gtcattggggc aacacggtta gcggggagag cacggggtag ccggagaagg 705

gcctctggag caggtctgga ggggccatgg ggcagtcctg ggtgtgggga cacagtcggg 765

ttgaccagg gctgtctccc tccagagcct ccctccggac aatgagtccc ccctcttgtc 825

tcccaccctg agattgggca tggggtgcgg tgtggggggc atgtgctgcc tgttgttatg 885

ggtttttttt gcgggggggg ttgctttttt ctgggggtctt tgagctccaa aaaataaaca 945

cttcctttga gggagagcac acctt

970

<210> 93

<211> 331

<212> PRT

<213> Homo sapiens

<400> 93

Met Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe

1	5	10	15
Arg Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn			
20	25	30	
Glu Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu			
35	40	45	
Ala Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala			
50	55	60	
Ile Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp			
65	70	75	80
Phe Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile			
85	90	95	
Glu Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly			
100	105	110	
Cys Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly			
115	120	125	
Ile Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr			
130	135	140	
Ser Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala			
145	150	155	160

Val Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser
165 170 175

Ala Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu
180 185 190

Lys Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser
195 200 205

Leu Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile
210 215 220

Arg Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr
225 230 235 240

Trp Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala
245 250 255

Gly Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr
260 265 270

Thr Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu
275 280 285

Ser Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu
290 295 300

Arg Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln
305 310 315 320

Ile Tyr Gln Arg Leu Asn Pro Cys His Thr His

325

330

<210> 94

<211> 2039

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (175)..(1167)

<400> 94

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cacactcttt caagagaagc ttccttgggt taagaaaaaa aacgaaccct tccagtcagg 120

tcagtgactg gagagctcca aggaaagtct ctcagtgacc tggtgctgg cacc atg 177

Met

1

gac tca gaa aag aaa cgc ttt act gaa gag gcc acc aaa tac ttc cgg 225

Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe Arg

5

10

15

gag aga gtc agc cca gtg cat ctg caa atc ctg ctg act aac aat gaa 273

Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn Glu

20	25	30	
gcc tgg aag aga ttc gtg act gcg gct gaa ttg ccc agg gat gag gca			321
Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu Ala			
35	40	45	
gat gct ctc tac gaa gct ctg aag aag ctt aga aca tat gca gct att			369
Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala Ile			
50	55	60	65
gag gac gaa tat gtg cag cag aaa gat gag cag ttt agg gaa tgg ttt			417
Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp Phe			
	70	75	80
ttg aaa gag ttt ccc caa gtc aag agg aag atc cag gag tcc ata gaa			465
Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile Glu			
	85	90	95
aag ctt cgt gcc ctt gca aat ggt att gaa gag gtc cac aga ggc tgc			513
Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly Cys			
100	105	110	
acc atc tcc aac gtg gtg tcc agc tcc act ggc gct gcc tct ggc atc			561
Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly Ile			
115	120	125	
atg tcc ctt gct ggt ctt gtt ttg gca cca ttt aca gca ggg acg agt			609
Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr Ser			
130	135	140	145

ctg gcc ctt act gca gct ggg gta ggg ctg gga gca gcg tct gct gtg 657
 Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala Val
 150 155 160

act ggg atc acc acc agc atc gtg gag cac tca tac aca tca tca gca 705
 Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser Ala
 165 170 175

gaa gct gaa gcc agc agg ctg act gca acc agc att gac cga ttg aag 753
 Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu Lys
 180 185 190

gta ttt aag gaa gtt atg cgt gac atc aca ccc aac tta ctt tcc ctt 801
 Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser Leu
 195 200 205

ctt aat aat tat tac gaa gcc aca caa acc att ggg agt gaa atc cgt 849
 Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile Arg
 210 215 220 225

gcc atc agg caa gcc aga gcc agg gcc cga ctc cct gtg acc acc tgg 897
 Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr Trp
 230 235 240

cga atc tca gct gga agt ggt ggt caa gca gag aga acg att gca ggc 945
 Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala Gly
 245 250 255

acc acc cgg gca gtg agc aga gga gcc cgg atc ctg agt gcg acc act 993
 Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr Thr
 260 265 270

tca ggc atc ttc ctt gca ctg gat gtg gtc aac ctt gta tac gag tca 1041
 Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu Ser
 275 280 285

aag cac ttg cat gag ggg gca aag tct gca tct gct gag gag ctg agg 1089
 Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu Arg
 290 295 300 305

cgg cag gct cag gag ctg gag gag aat cta atg gag ctc act cag atc 1137
 Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln Ile
 310 315 320

tat cag cgt ctg aat cca tgc cat acc cac tgaccccaga ccagtgcagc 1187
 Tyr Gln Arg Leu Asn Pro Cys His Thr His
 325 330

cagcagggga ggtgagccat acacaggcca cgacaaaatg caggcatttt attaggggga 1247

taaagagggc aaggtaaagt ttatggagct gagtgtagt gactttggca tttctgtagc 1307

tgagcacagc aggggagggg ttaatgcaga tggcaagtgc accaaggaga aggcaggaat 1367

gctggagcct ggaataaggg aggagagggg actggagagt gtggggaata ggaagaagaa 1427

atttccttta gactaacgaa tatattgggg ggaggaatag aggggaggtg tgcaggaacc 1487

agcaatgaga aggccaggaa aagaaagagc tgaaaatgca gaaagccgaa gagttagaac 1547
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 tctctaaaaa cccaaacatc ctggagagta tgcgagaacc taccaagaaa aacagtctca 1907
 ttactcatat acagcaggca aagagacaga aaattaactg aaaagcagtt tagagactgg 1967
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<210> 95

<211> 407

<212> PRT

<213> Homo sapiens

<400> 95

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Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg			
35	40	45	
Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr			
50	55	60	
Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu			
65	70	75	80
Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly			
85	90	95	
His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu			
100	105	110	
Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe			
115	120	125	
Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser			
130	135	140	
Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg			
145	150	155	160

Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr
165 170 175

Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr
180 185 190

Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys
195 200 205

Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr
210 215 220

Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys
225 230 235 240

Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg
245 250 255

Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu
260 265 270

Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp
275 280 285

Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly
290 295 300

Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu
305 310 315 320

Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu
325 330 335

Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser
340 345 350

Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser
355 360 365

Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu
370 375 380

Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe
385 390 395 400

Val Cys Lys Tyr Lys Leu Leu
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<210> 96

<211> 1409

<212> DNA

<213> Homo sapiens

<220>

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<222> (181)..(1401)

<400> 96

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tttgccctgg gaaatagtaa ccctgccaaa tacatcagct tgtaggagac agaggatgtg 180

atg gag ctg ctt gaa gaa gat ctc aca tgc cct att tgt tgt agt ctg 228

Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu

1 5 10 15

ttt gat gat cca cgg gtt ttg cct tgc tcc cac aac ttc tgc aaa aaa 276

Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys

20 25 30

tgc tta gaa ggt atc tta gaa ggg agt gtg cgg aat tcc ttg tgg aga 324

Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg

35 40 45

cca gct cca ttc aag tgt cct aca tgc cgt aag gaa act tca gct act 372

Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr

50 55 60

gga att aat agc ctg cag gtt aat tac tcc ctg aag ggt att gtg gaa 420

Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu

65 70 75 80

aag tat aac aag atc aag atc tct ccc aaa atg cca gta tgc aaa gga 468

Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly

85

90

95

cac ttg ggg cag cct ctc aac att ttc tgc ctg act gat atg cag ctg 516

His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu

100

105

110

att tgt ggg atc tgt gct act cgt ggg gag cac acc aaa cat gtc ttc 564

Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe

115

120

125

tgt tct att gaa gat gcc tat gct cag gaa agg gat gcc ttt gag tcc 612

Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser

130

135

140

ctc ttc cag agc ttt gag acc tgg cgt cgg gga gat gct ctt tct cgc 660

Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg

145

150

155

160

ttg gat acc ttg gaa act agt aag agg aaa tcc cta cag tta ctg act 708

Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr

165

170

175

aaa gat tca gat aaa gtg aag gaa ttt ttt gag aag tta caa cac aca 756

Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr

180

185

190

ctg gat caa aag aag aat gaa att ctg tct gac ttt gag acc atg aaa 804

Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys

195

200

205

ctt gct gtt atg caa gca tat gac cca gag atc aac aaa ctc aac acc 852

Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr

210

215

220

atc ttg cag gag caa cgg atg gcc ttt aac att gct gag gct ttc aaa 900

Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys

225

230

235

240

gat gtg tca gaa ccc att gta ttt ctg caa cag atg cag gag ttt aga 948

Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg

245

250

255

gag aaa atc aaa gta atc aag gaa act cct tta cct ccc tct aat ttg 996

Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu

260

265

270

cct gca agc cct tta atg aag aac ttt gat acc agt cag tgg gaa gac 1044

Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp

275

280

285

ata aaa cta gtc gat gtg gat aaa ctt tct ttg cct caa gac act ggc 1092

Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly

290

295

300

aca ttc att agc aag att ccc tgg agc ttt tat aag tta ttt ttg cta 1140

Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu

305

310

315

320

atc ctt ctg ctt ggc ctt gtc att gtc ttt ggt cct acc atg ttc cta 1188
 Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu

325

330

335

gaa tgg tca tta ttt gat gac ctg gca act tgg aaa ggc tgt ctt tca 1236
 Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser

340

345

350

aac ttc agt tcc tat ctg act aaa aca gcc gat ttc ata gaa caa tca 1284
 Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser

355

360

365

gtt ttt tac tgg gaa cag gtg aca gat ggg ttt ttc att ttc aat gaa 1332
 Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu

370

375

380

aga ttc aag aat ttt act ttg gtg gta ctg aac aat gtg gca gaa ttt 1380
 Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe

385

390

395

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gtg tgc aaa tat aaa cta tta taaaatcg 1409
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405

<210> 97

<211> 465

<212> PRT

<213> Homo sapiens

<400> 97

Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys

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Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly

20 25 30

His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser

35 40 45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala

50 55 60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu

65 70 75 80

Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His

85 90 95

Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys

100 105 110

Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu

115 120 125

Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val

130 135 140

Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser
145 150 155 160

Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg
165 170 175

Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu
180 185 190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr
195 200 205

Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn
210 215 220

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser
225 230 235 240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp
245 250 255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr
260 265 270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg
275 280 285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu
290 295 300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln
305 310 315 320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val
325 330 335

Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp
340 345 350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val
355 360 365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr
370 375 380

Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro
385 390 395 400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu
405 410 415

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys
420 425 430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro
435 440 445

Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly
336/754

450

455

460

Asp

465

<210> 98

<211> 1940

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (477)..(1871)

<400> 98

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ccttggaagg aggggagccc catctcccca gaagagcagt gaccccagca gagaggggcc 180

tggtgtatca ctggaggaaa tagcctgcc aagaaatcac gtcttcagaa gaagttctgt 240

gtggcttcaa gagactgac aaattgtgag aggaaaacag cctaccgggt cctcttttct 300

tcaatacaaa atgagataat aggggttga aggaaaacct tcaagaccta tggaagtcag 360

ttgcagccag ctcacacat agaggtgcag gtgaggtgta tttcatcac ggtggaaaat 420

tctggctgct tcattccat ctctagagcc aatattggag cttttcaata aaagct atg 479

Met

1

gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc 527

Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser

5

10

15

atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac 575

Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His

20

25

30

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa 623

Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln

35

40

45

aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca 671

Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro

50

55

60

65

ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att 719

Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile

70

75

80

gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga 767

Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly

85

90

95

gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg 815
 Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp

100

105

110

cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt 863
 Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val

115

120

125

gaa gac gta tgc cag ggc tac aag gaa aag ctc cag gaa gct gtg aca 911
 Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val Thr

130

135

140

145

aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca 959
 Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr

150

155

160

gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa 1007
 Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln

165

170

175

aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa 1055
 Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu

180

185

190

gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg 1103
 Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu

195

200

205

agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa 1151

Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu
 210 215 220 225

ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc 1199
 Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala
 230 235 240

cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct 1247
 Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala
 245 250 255

gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg 1295
 Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met
 260 265 270

tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt 1343
 Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser
 275 280 285

cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta 1391
 His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu
 290 295 300 305

att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag 1439
 Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu
 310 315 320

aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg 1487
 Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu

325	330	335	
ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt			1535
Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val			
340	345	350	
ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag			1583
Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln			
355	360	365	
agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc			1631
Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu			
370	375	380	385
agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act			1679
Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr			
390	395	400	
tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac			1727
Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp			
405	410	415	
tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac			1775
Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His			
420	425	430	
atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat			1823
Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr			
435	440	445	

ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac 1871

Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp

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taagggcag 1940

<210> 99

<211> 465

<212> PRT

<213> Homo sapiens

<400> 99

Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys

1 5 10 15

Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly

20 25 30

His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser

35 40 45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala

50 55 60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu

65	70	75	80
Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His			
85	90	95	
Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys			
100	105	110	
Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu			
115	120	125	
Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val			
130	135	140	
Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser			
145	150	155	160
Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg			
165	170	175	
Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu			
180	185	190	
Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr			
195	200	205	
Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn			
210	215	220	

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser
225 230 235 240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp
245 250 255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr
260 265 270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg
275 280 285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu
290 295 300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln
305 310 315 320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val
325 330 335

Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp
340 345 350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val
355 360 365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr
370 375 380

Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro
 385 390 395 400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu
 405 410 415

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys
 420 425 430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro
 435 440 445

Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly
 450 455 460

Asp

465

<210> 100

<211> 1940

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (477).. (1871)

<400> 100

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caccaaattct cagaagattc agaacttaga tgagtggggc ccaggacagg aaccctggag 120

ccttggaagg aggggagccc catctcccca gaagagcagt gacccagca gagaggggcc 180

tgggtgtatca ctggaggaaa tagcctgcc aggaatacac gtcttcagaa gaagttctgt 240

gtggcttcaa gagactgata aaattgtgag aggaaaacag cctaccggt cctcttttct 300

tcaatacaaaa atgagataat aggggttgga aggaaaacct tcaagaccta tggaagtcag 360

ttgcagccag ctcatcacat agaggtgcag gtgaggtgta ttttcatcac ggtggaaaat 420

tctggctgct tcatctccat ctctagagcc aatattggag cttttcaata aaagct atg 479

Met

1

gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc 527

Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser

5

10

15

atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac 575

Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His

20

25

30

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa 623

Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln

35	40	45	
aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca	671		
Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro			
50	55	60	65
ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att	719		
Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile			
	70	75	80
gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga	767		
Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly			
	85	90	95
gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg	815		
Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp			
	100	105	110
cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt	863		
Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val			
	115	120	125
gaa gac gta tgc cag ggc tac aag gaa aag ctc cag aaa gct gtg aca	911		
Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val Thr			
	130	135	140
aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca	959		
Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr			
	150	155	160

gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa 1007

Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln

165

170

175

aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa 1055

Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu

180

185

190

gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg 1103

Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu

195

200

205

agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa 1151

Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu

210

215

220

225

ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc 1199

Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala

230

235

240

cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct 1247

Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala

245

250

255

gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg 1295

Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met

260

265

270

tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt 1343
 Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser

275

280

285

cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta 1391
 His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu

290

295

300

305

att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag 1439
 Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu

310

315

320

aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg 1487
 Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu

325

330

335

ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt 1535
 Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val

340

345

350

ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag 1583
 Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln

355

360

365

agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc 1631
 Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu

370

375

380

385

agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act 1679

Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr
390 395 400

tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac 1727
Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp
405 410 415

tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac 1775
Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His
420 425 430

atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat 1823
Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr
435 440 445

ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac 1871
Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp
450 455 460 465

taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataatccca 1931

taagggcag 1940

<210> 101

<211> 685

<212> PRT

<213> Homo sapiens

<400> 101

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1 5 10 15

Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser Lys Lys

20 25 30

Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln Ser Gln

35 40 45

Ala Gln Val Pro Pro Ala Ala Pro His His His His His His Ser His

50 55 60

Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr Gly Lys

65 70 75 80

Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala Lys Cys

85 90 95

Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala Lys Ile

100 105 110

Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys Ile Asp

115 120 125

Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val Val Gln

130 135 140

Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu Leu Glu

145	150	155	160
Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg Lys Val			
	165	170	175
Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val Ser Gly			
	180	185	190
Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu Lys Leu			
	195	200	205
Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly Asp Phe			
	210	215	220
Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg Thr Ile			
	225	230	235
			240
Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys Gln Gly			
	245	250	255
His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met Tyr Thr			
	260	265	270
Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys Glu Thr			
	275	280	285
Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser Leu Leu			
	290	295	300

Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn Pro Glu
305 310 315 320

Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe Leu Gln
325 330 335

Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr Val Pro
340 345 350

Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys Ala Ala
355 360 365

Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile Asp Thr
370 375 380

His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu Arg His
385 390 395 400

Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His Arg Thr
405 410 415

Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser Gly Thr
420 425 430

Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg Met Ile
435 440 445

Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys Leu Glu
450 455 460

Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val Leu Arg
465 470 475 480

Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys Glu Gln
485 490 495

Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn
500 505 510

Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu
515 520 525

Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Val
530 535 540

His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp
545 550 555 560

Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser
565 570 575

His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val
580 585 590

Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser
595 600 605

Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn

610	615	620	
Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu Glu			
625	630	635	640

Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg		
645	650	655

Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys Asn Arg		
660	665	670

Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn		
675	680	685

<210> 102

<211> 2783

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (128).. (2182)

<400> 102

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cggccggctc ggacgtgtga ccgcgcctag ggggtggcag cgggcagtg cggggcggcaa 120

ggcgacc atg gag ctt ttg cgg act atc acc tac cag cca gcc gcc agc 169

Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser

1

5

10

acc aaa atg tgc gag cag gcg ctg ggc aag ggt tgc gga gca gac tcg 217

Thr Lys Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser

15

20

25

30

aag aag aag cgg ccg ccg cag ccc ccc gag gaa tcg cag cca cct cag 265

Lys Lys Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln

35

40

45

tcc cag gcg caa gtg ccc ccg gcg gcc cct cac cac cat cac cac cat 313

Ser Gln Ala Gln Val Pro Pro Ala Ala Pro His His His His His His

50

55

60

tcg cac tcg ggg ccg gag atc tcg cgg att atc gtc gac ccc acg act 361

Ser His Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr

65

70

75

ggg aag cgc tac tgc cgg ggc aaa gtg ctg gga aag ggt ggc ttt gca 409

Gly Lys Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala

80

85

90

aaa tgt tac gag atg aca gat ttg aca aat aac aaa gtc tac gcc gca 457

Lys Cys Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala

95

100

105

110

aaa att att cct cac agc aga gta gct aaa cct cat caa agg gaa aag 505

Lys Ile Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys	
115 120 125	
att gac aaa gaa ata gag ctt cac aga att ctt cat cat aag cat gta	553
Ile Asp Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val	
130 135 140	
gtg cag ttt tac cac tac ttc gag gac aaa gaa aac att tac att ctc	601
Val Gln Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu	
145 150 155	
ttg gaa tac tgc agt aga agg tca atg gct cat att ttg aaa gca aga	649
Leu Glu Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg	
160 165 170	
aag gtg ttg aca gag cca gaa gtt cga tac tac ctc agg cag att gtg	697
Lys Val Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val	
175 180 185 190	
tct gga ctg aaa tac ctt cat gaa caa gaa atc ttg cac aga gat ctc	745
Ser Gly Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu	
195 200 205	
aaa cta ggg aac ttt ttt att aat gaa gcc atg gaa cta aaa gtt ggg	793
Lys Leu Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly	
210 215 220	
gac ttc ggt ctg gca gcc agg cta gaa ccc ttg gaa cac aga agg aga	841
Asp Phe Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg	

225	230	235	
acg ata tgt ggt acc cca aat tat ctc tct cct gaa gtc ctc aac aaa			889
Thr Ile Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys			
240	245	250	
caa gga cat ggc tgt gaa tca gac att tgg gcc ctg ggc tgt gta atg			937
Gln Gly His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met			
255	260	265	270
tat aca atg tta cta ggg agg ccc cca ttt gaa act aca aat ctc aaa			985
Tyr Thr Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys			
275	280	285	
gaa act tat agg tgc ata agg gaa gca agg tat aca atg ccg tcc tca			1033
Glu Thr Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser			
290	295	300	
ttg ctg gct cct gcc aag cac tta att gct agt atg ttg tcc aaa aac			1081
Leu Leu Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn			
305	310	315	
cca gag gat cgt ccc agt ttg gat gac atc att cga cat gac ttt ttt			1129
Pro Glu Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe			
320	325	330	
ttg cag ggc ttc act ccg gac aga ctg tct tct agc tgt tgt cat aca			1177
Leu Gln Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr			
335	340	345	350

gtt cca gat ttc cac tta tca agc cca gct aag aat ttc ttt aag aaa 1225

Val Pro Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys

355

360

365

gca gct gct gct ctt ttt ggt ggc aaa aaa gac aaa gca aga tat att 1273

Ala Ala Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile

370

375

380

gac aca cat aat aga gtg tct aaa gaa gat gaa gac atc tac aag ctt 1321

Asp Thr His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu

385

390

395

agg cat gat ttg aaa aag act tca ata act cag caa ccc agc aaa cac 1369

Arg His Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His

400

405

410

agg aca gat gag gag ctc cag cca cct acc acc aca gtt gcc agg tct 1417

Arg Thr Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser

415

420

425

430

gga aca ccc gca gta gaa aac aag cag cag att ggg gat gct att cgg 1465

Gly Thr Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg

435

440

445

atg ata gtc aga ggg act ctt ggc agc tgt agc agc agc agt gaa tgc 1513

Met Ile Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys

450

455

460

ctt gaa gac agt acc atg gga agt gtt gca gac aca gtg gca agg gtt 1561
 Leu Glu Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val

465

470

475

ctt cgg gga tgt ctg gaa aac atg ccg gaa gct gat tgc att ccc aaa 1609
 Leu Arg Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys

480

485

490

gag cag ctg agc aca tca ttt cag tgg gtc acc aaa tgg gtt gat tac 1657
 Glu Gln Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr

495

500

505

510

tct aac aaa tat ggc ttt ggg tac cag ctc tca gac cac acc gtc ggt 1705
 Ser Asn Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly

515

520

525

gtc ctt ttc aac aat ggt gct cac atg agc ctc ctt cca gac aaa aaa 1753
 Val Leu Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys

530

535

540

aca gtt cac tat tac gca gag ctt ggc caa tgc tca gtt ttc cca gca 1801
 Thr Val His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala

545

550

555

aca gat gct cct gag caa ttt att agt caa gtg acg gtg ctg aaa tac 1849
 Thr Asp Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr

560

565

570

ttt tct cat tac atg gag gag aac ctc atg gat ggt gga gat ctg cct 1897

Phe Ser His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro
 575 580 585 590

agt gtt act gat att cga aga cct cgg ctc tac ctc ctt cag tgg cta 1945
 Ser Val Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu
 595 600 605

aaa tct gat aag gcc cta atg atg ctc ttt aat gat ggc acc ttt cag 1993
 Lys Ser Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln
 610 615 620

gtg aat ttc tac cat gat cat aca aaa atc atc atc tgt agc caa aat 2041
 Val Asn Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn
 625 630 635

gaa gaa tac ctt ctc acc tac atc aat gag gat agg ata tct aca act 2089
 Glu Glu Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr
 640 645 650

ttc agg ctg aca act ctg ctg atg tct ggc tgt tca tca gaa tta aaa 2137
 Phe Arg Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys
 655 660 665 670

aat cga atg gaa tat gcc ctg aac atg ctc tta caa aga tgt aac 2182
 Asn Arg Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
 675 680 685

tgaaagactt ttcgaatgga ccctatggga ctctctttt ccactgtgag atctacaggg 2242

aaccctaaag aatgatctag agtatgttga agaagatgga catgtggtgg tacgaaaaca 2302
attccctgtt ggcctgctgg actgggtgga accagaacag gctaaggcat acagttcttg 2362
actttggaca atccaagagt gaaccagaat gcagttttcc ttgagatacc tgttttaaaa 2422
ggtttttcag acaattttgc agaaaggtgc attgattctt aaattctctc tgttgagagc 2482
atttcagcca gaggactttg gaactgtgaa tatacttcct gaaggggagg gagaaggag 2542
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ctatggccat atataatttt ttttcattaa ttttgaaga tacttgtggc tggaaaagtg 2662
cattccttgt taataaactt tttatttatt acagcccaaa gagcagtatt tattatcaaa 2722
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g 2783

<210> 103

<211> 161

<212> PRT

<213> Homo sapiens

<400> 103

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5

10

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Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr
20 25 30

Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val
35 40 45

Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln
50 55 60

Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr
65 70 75 80

Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met Cys Cys
85 90 95

Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly
100 105 110

Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile
115 120 125

Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val
130 135 140

Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg
145 150 155 160

Leu

<210> 104

<211> 1589

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)..(552)

<400> 104

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ggcggtaaaa atg tcg gtt cca gga cct tac cag gcg gcc act ggg cct tcc 111

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser

1

5

10

tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159

Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn

15

20

25

30

agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207

Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly

35

40

45

ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat 255

Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr

50	55	60	
acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg			303
Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr			
65	70	75	
gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct atc caa atg			351
Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met			
80	85	90	
tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac			399
Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn			
95	100	105	110
gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg			447
Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly			
115	120	125	
tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag			495
Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln			
130	135	140	
gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac			543
Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr			
145	150	155	
aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg			592
Lys Arg Leu			
160			

aagtcctttc cacctctcat ccagcttcac gcctgggtgga ggttctgccc tgggtggtctc 652

acctctccag ggggccacc ttcatgtctt cttttggggg gaatacgtcg caaaactaac 712

aaatctccaa accccagaaa ttgctgcttg gagtcgtgca taggacttgc aaagacattc 772

cccttgagtg tcagttccac ggtttcctgc ctccctgaga ccctgagtcc tgccatctaa 832

ctgtgatcat tgccctatcc gaatatcttc ctgtgatctg ccatcagtgg ctcttttttc 892

ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccttattt 952

ttgaggctgt tctgccaga gctcggctga accagccttt agtgcctacc attatcttat 1012

ccgtctcttc ccgtccctga tgacaaagat cttgccttac agactttaca ggcttggtt 1072

tgagattctg taactgcaga cttcattagc acacagattc actttaattt ctttaatttt 1132

tttttaata caaggagggg gctattaaca ccagtacag acatatccac aaggtcgtaa 1192

atgcatgcta gaaaaatagg gctggatctt atcactgccc tgtctcccct tgtttctctg 1252

tgccagatct tcagtgcacc ttccataca gggatTTTTT tctcatagag taattatatg 1312

aacagTTTTT atgacctct tttggtctga aatactttcg aacagaattt ctttttttta 1372

aaaaaaaaca gagatggggt cttactatgt tgcccaggct ggtgtcgaac tcctgggctc 1432

aagcgatcct tctgccttgg cctcccgaag tgctgggatt gcaggcataa gctaccatgc 1492

tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaatgat 1552

tggtgtcatt ttcccatttg ccaatgtagt ctcactt 1589

<210> 105

<211> 161

<212> PRT

<213> Homo sapiens

<400> 105

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser Ser Ala

1 5 10 15

Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr

20 25 30

Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val

35 40 45

Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln

50 55 60

Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr

65 70 75 80

Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met Cys Cys

85

90

95

Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly

100

105

110

Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile

115

120

125

Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val

130

135

140

Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg

145

150

155

160

Leu

<210> 106

<211> 1589

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)..(552)

<400> 106

cctttttctcg gggcgccccga aggccagctc agacctcccg gctcgacagg cggcgcgggc 60

ggcggtaaa atg tgc gtt cca gga cct tac cag gcg gcc act ggg cct tcc 111

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser

1

5

10

tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac 159

Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn

15

20

25

30

agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg 207

Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly

35

40

45

ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tgc tat tat 255

Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr

50

55

60

acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg 303

Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr

65

70

75

gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct gtc caa atg 351

Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met

80

85

90

tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac 399

Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn

95

100

105

110

gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg 447
 Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly

115 120 125

tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag 495
 Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln

130 135 140

gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac 543
 Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr

145 150 155

aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg 592
 Lys Arg Leu

160

aagtcctttc cacctctcat ccagcttcac gcctggtgga ggttctgccc tgggtggtctc 652

acctctccag ggggccacc ttcattgtctt cttttggggg gaatacgtcg caaaactaac 712

aaatctccaa accccagaaa ttgctgcttg gagtcgtgca taggacttgc aaagacattc 772

cccttgagtg tcagttccac ggtttcctgc ctccctgaga ccctgagtcc tgccatctaa 832

ctgtgatcat tgccctatcc gaatatcttc ctgtgatctg ccatcagtgg ctcttttttc 892

ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccttattt 952

ttgaggctgt tctgcccaga gctcggctga accagccttt agtgccctacc attatcttat 1012

ccgtctcttc ccgtccctga tgacaaagat cttgccttac agactttaca ggcttggctt 1072
 tgagattctg taactgcaga cttcattagc acacagattc actttaattt ctttaatttt 1132
 tttttaaata caaggagggg gctattaaca cccagtacag acatatccac aaggtcgtaa 1192
 atgcatgcta gaaaaatagg gctggatctt atcactgccc tgtctcccct tgtttctctg 1252
 tgccagatct tcagtgcctt tttccataca gggatttttt tctcatagag taattatatg 1312
 aacagttttt atgacctcct tttggcttga aatactttcg aacagaattt ctttttttta 1372
 aaaaaaaca gagatggggg cttactatgt tgcccaggct ggtgtcgaac tcctgggctc 1432
 aagcgatcct tctgccttgg cctcccgaag tgctgggatt gcaggcataa gctaccatgc 1492
 tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaagat 1552
 tgggtgtcatt ttcccatttg ccaatgtagt ctcaatt 1589

<210> 107

<211> 249

<212> PRT

<213> Homo sapiens

<400> 107

Met Ala Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val

1	5	10	15
Leu Asp Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val			
20	25	30	
Val Thr Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys			
35	40	45	
Phe Lys Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn			
50	55	60	
Ser Gly Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu			
65	70	75	80
Gln Pro Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met			
85	90	95	
Val Gln Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val			
100	105	110	
Trp Lys Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys			
115	120	125	
Val Phe Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro			
130	135	140	
Ser Lys Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro			
145	150	155	160

Lys Pro His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met
165 170 175

Glu Glu Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu
180 185 190

Asn Arg His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His
195 200 205

Ser Asp Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val
210 215 220

Thr Ser Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile
225 230 235 240

Gly Phe Phe Leu Gly Lys Phe Ile Leu
245

<210> 108

<211> 1595

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (232).. (978)

<400> 108

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 gaccacgcgg gtggcccacc gaaccggtga cacagcggca ggcgttaggg ctcgaggacc 120
 gcgagcctgg cctcgtccta gagctcggcc gagccgtcgc cgccgtcgtc ccccgccccc 180
 agtcagcaaa ccgccgcgc gggcgcgccc ccgtctctgc ctgtctctcc g atg gcg 237
 Met Ala
 1
 tcc gcc tca ggg gcc atg gcg aag cac gag cag atc ctg gtc ctc gat 285
 Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val Leu Asp
 5 10 15
 ccg ccc aca gac ctc aaa ttc aaa ggc ccc ttc aca gat gta gtc act 333
 Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val Val Thr
 20 25 30
 aca aat ctt aaa ttg cga aat cca tcg gat aga aaa gtg tgt ttc aaa 381
 Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys Phe Lys
 35 40 45 50
 gtg aag act aca gca cct cgc cgg tac tgt gtg agg ccc aac agt gga 429
 Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly
 55 60 65
 att att gac cca ggg tca act gtg act gtt tca gta atg cta cag ccc 477
 Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu Gln Pro
 70 75 80

ttt gac tat gat ccg aat gaa aag agt aaa cac aag ttt atg gta cag 525

Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val Gln

85

90

95

aca att ttt gct cca cca aac act tca gat atg gaa gct gtg tgg aaa 573

Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val Trp Lys

100

105

110

gag gca aaa cct gat gaa tta atg gat tcc aaa ttg aga tgc gta ttt 621

Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys Val Phe

115

120

125

130

gaa atg ccc aat gaa aat gat aaa ttg aat gat atg gaa cct agc aaa 669

Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro Ser Lys

135

140

145

gct gtt cca ctg aat gca tct aag caa gat gga cct atg cca aaa cca 717

Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro Lys Pro

150

155

160

cac agt gtt tca ctt aat gat acc gaa aca agg aaa cta atg gaa gag 765

His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met Glu Glu

165

170

175

tgt aaa aga ctt cag gga gaa atg atg aag cta tca gaa gaa aat cgg 813

Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu Asn Arg

180

185

190

cac ctg aga gat gaa ggt tta agg ctc aga aag gta gca cat tcg gat 861
 His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His Ser Asp
 195 200 205 210

aaa cct gga tca acc tca act gca tcc ttc aga gat aat gtc acc agt 909
 Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val Thr Ser
 215 220 225

cct ctt cct tca ctt ctt gtt gta att gca gcc att ttc att gga ttc 957
 Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile Gly Phe
 230 235 240

ttt cta ggg aaa ttc atc ttg tagagtgaag catgcagagt gctgtttcct 1008
 Phe Leu Gly Lys Phe Ile Leu
 245

tttttttttt tctcttgacc agaaaaagat ttgtttacct accatttcac tggtagtatg 1068

gcccacggtg accatttttt tgtgtgtaca gcgtcatata ggctttgcct ttaatgatct 1128

cttacggtta gaaaacacaa taaaaacaaa ctgttcggt actggacagg ttgtatatta 1188

ccagatcatc actagcagat gtcagttgca cattgagtcc tttatgaaat tcataaataa 1248

agaattgttc tttctttgtg gttttaataa gagtccaaga attgttcaga gtcttgtaaa 1308

tgttatttta ataatccctt taaattttat ctgttgctgt tacctcttga aatatgattt 1368

atttagattg ctaatcccac tcattcagga aatgccaaaga ggtattcctt ggggaaatgg 1428

tgcctcttac agtgtaaatt tttcctcctt tacctttgct aatatcatgg cagaattttt 1488

cttatccctt gtgaggcagt tgttgactga gtttttcac cttacaatcc tgtcccatgg 1548

tatttaacat aaaaaaaaaat aaaactgtta acagattcctt gctcgat 1595

<210> 109

<211> 540

<212> PRT

<213> Homo sapiens

<400> 109

Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val

1 5 10 15

Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln

20 25 30

Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser

35 40 45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln

50 55 60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser

65 70 75 80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu
85 90 95

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro
100 105 110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
115 120 125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser
130 135 140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp
145 150 155 160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn
165 170 175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro
180 185 190

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
195 200 205

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
210 215 220

Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
225 230 235 240

Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His
245 250 255

Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu
260 265 270

Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln
275 280 285

Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro
290 295 300

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser
305 310 315 320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu
325 330 335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly
340 345 350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys
355 360 365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys
370 375 380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala
379/754

385	390	395	400
Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg			
405	410	415	
Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu			
420	425	430	
Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg			
435	440	445	
Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu			
450	455	460	
Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp			
465	470	475	480
Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val			
485	490	495	
Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly			
500	505	510	
Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly			
515	520	525	
Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu			
530	535	540	

<210> 110

<211> 1810

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (102)..(1721)

<400> 110

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gaggaccacac ctctgagtgt ccagtggtea gttgccccag g atg ggg acc aca gcc 116

Met Gly Thr Thr Ala

1

5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164

Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser

10

15

20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212

Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His

25

30

35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260

Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg

40

45

50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308

Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe

55

60

65

gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 356

Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro

70

75

80

85

ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa 404

Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu

90

95

100

gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg 452

Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu

105

110

115

ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca 500

Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro

120

125

130

ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag 548

Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln

135

140

145

cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat 596

His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp

150

155

160

165

ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc 644

Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys	
170	175 180
ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag	692
Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln	
185	190 195
tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg	740
Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu	
200	205 210
gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc	788
Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg	
215	220 225
cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt	836
Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys	
230	235 240 245
gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg	884
Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg	
250	255 260
cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca	932
Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro	
265	270 275
cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg	980
His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser	

280	285	290	
ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc			1028
Gly Leu Glu Leu P			
ro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile			
295	300	305	
aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg			1076
Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu			
310	315	320	325
cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg			1124
Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu			
	330	335	340
gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt			1172
Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys			
	345	350	355
aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag			1220
Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu			
	360	365	370
tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc			1268
Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser			
	375	380	385
cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat			1316
Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr			

390	395	400	405	
gac cgg gac atc ttg acc att gac atc ggt cga gtc acc ccc aac ctc				1364
Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg Val Thr Pro Asn Leu				
	410	415	420	
atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat				1412
Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His				
	425	430	435	
att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca				1460
Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro				
	440	445	450	
ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc				1508
Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile				
	455	460	465	
aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc				1556
Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu				
470	475	480	485	
tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc				1604
Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile				
	490	495	500	
aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc				1652
Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala				
	505	510	515	

aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc 1700

Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser

520

525

530

acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga 1751

Thr Ser Glu Pro Lys Glu Glu

535

540

tggggggaac cccaccctgc cccacccatc tgaacactca ttacactaaa cacctcttg 1810

<210> 111

<211> 540

<212> PRT

<213> Homo sapiens

<400> 111

Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val

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Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln

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30

Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser

35

40

45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln

50

55

60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser
65 70 75 80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu
85 90 95

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro
100 105 110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
115 120 125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser
130 135 140

Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp
145 150 155 160

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn
165 170 175

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro
180 185 190

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
195 200 205

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg

210	215	220	
Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala			
225	230	235	240
Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His			
	245	250	255
Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu			
	260	265	270
Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln			
	275	280	285
Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro			
	290	295	300
Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser			
305	310	315	320
Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu			
	325	330	335
Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly			
	340	345	350
Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys			
	355	360	365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys
370 375 380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala
385 390 395 400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg
405 410 415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu
420 425 430

Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg
435 440 445

Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu
450 455 460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp
465 470 475 480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val
485 490 495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly
500 505 510

Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly
515 520 525

Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu

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535

540

<210> 112

<211> 1810

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (102)..(1721)

<400> 112

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gaggacccac ctctgagtgt ccagtgggtca gttgccccag g atg ggg acc aca gcc 116

Met Gly Thr Thr Ala

1

5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164

Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser

10

15

20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212

Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His

25

30

35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260
Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg

40

45

50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308
Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe

55

60

65

gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 356
Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro

70

75

80

85

ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa 404
Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu

90

95

100

gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg 452
Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu

105

110

115

ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca 500
Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro

120

125

130

ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag 548
Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln

135

140

145

cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat 596

His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp
 150 155 160 165

ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc 644
 Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys
 170 175 180

ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag 692
 Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln
 185 190 195

tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg 740
 Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu
 200 205 210

gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc 788
 Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg
 215 220 225

cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt 836
 Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys
 230 235 240 245

gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg 884
 Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg
 250 255 260

cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca 932
 Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro

265	270	275	
cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg			980
His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser			
280	285	290	
ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc			1028
Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile			
295	300	305	
aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg			1076
Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu			
310	315	320	325
cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg			1124
Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu			
330	335	340	
gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt			1172
Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys			
345	350	355	
aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag			1220
Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu			
360	365	370	
tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc			1268
Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser			
375	380	385	

cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat 1316

Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr

390 395 400 405

gac cgg gac atc ttg acc att gac atc agt cga gtc acc ccc aac ctc 1364

Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg Val Thr Pro Asn Leu

410 415 420

atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat 1412

Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His

425 430 435

att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca 1460

Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro

440 445 450

ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc 1508

Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile

455 460 465

aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc 1556

Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu

470 475 480 485

tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc 1604

Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile

490 495 500

aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc 1652

Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala

505

510

515

aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc 1700

Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser

520

525

530

acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga 1751

Thr Ser Glu Pro Lys Glu Glu

535

540

tggggggaac cccaccctgc cccacccatc tgaacactca ttacactaaa cacctcttg 1810

<210> 113

<211> 382

<212> PRT

<213> Homo sapiens

<400> 113

Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu Asp Lys Val Gln Ala

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Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe

20

25

30

Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu

35

40

45

395/754

Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val
50 55 60

Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu
65 70 75 80

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val
85 90 95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu
100 105 110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys
115 120 125

Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys
130 135 140

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu
145 150 155 160

Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile
165 170 175

Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
180 185 190

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile

195	200	205
Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn		
210	215	220
Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val		
225	230	235 240
Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro		
	245	250 255
Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser		
	260	265 270
Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu		
	275	280 285
Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln		
	290	295 300
Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met		
305	310	315 320
Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp		
	325	330 335
Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu		
	340	345 350

Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser
 355 360 365

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile
 370 375 380

<210> 114

<211> 3074

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (201)..(1346)

<400> 114

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aacagcagcg gagttttaaa ctttaaatac acaggtctga gtgcctgaac ttgccttttc 120

attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac tttaagcaa 180

aagagtgggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233

Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu

1

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10

gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281

Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser

15	20	25	
gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca			329
Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser			
30	35	40	
gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct			377
Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro			
45	50	55	
ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg			425
Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val			
60	65	70	75
cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg			473
Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu			
80	85	90	
tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac			521
Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn			
95	100	105	
aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg			569
Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val			
110	115	120	
gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att			617
Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile			
125	130	135	

gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac 665

Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr

140 145 150 155

atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg 713

Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu

160 165 170

atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc 761

Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys

175 180 185

aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc 809

Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro

190 195 200

acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg 857

Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val

205 210 215

tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc 905

Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly

220 225 230 235

gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt 953

Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser

240 245 250

ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat 1001
 Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr

255

260

265

ttc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct 1049
 Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro

270

275

280

cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc 1097
 Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg

285

290

295

aat tac aac aag caa gca agt gag caa acc tgg gct aat tac agt gca 1145
 Asn Tyr Asn Lys Gln Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala

300

305

310

315

gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat 1193
 Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His

320

325

330

gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta 1241
 Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu

335

340

345

gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct 1289
 Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro

350

355

360

tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac 1337

Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp

365

370

375

ctg gag atc tagatacagg cttgaaagca tcaagattcc actcaattgt 1386

Leu Glu Ile

380

ggagaagaaa aaaggtgctg tagaaagtgc accaggtggt aattttgatc cggtggaggt 1446

ggtactcaac agccttattc atgaggctta gaaaacacaa agacattaga atacctaggt 1506

tcactggggg tgtatggggt agatgggtgg agagggaggg gataagagag gtgcatgttg 1566

gtatttaaag tagtggattc aaagaactta gattataaat aagagttcca ttaggtgata 1626

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gagcgggtgg taattgtggc taaatatattt tgttttacca agaaactgaa ataattctgg 1746

ccaggaataa atacttcttg aacatcttag gtcttttcaa caagaaaaag acagaggatt 1806

gtccttaagt ccctgctaaa acattccatt gttaaaattt gcactttgaa ggtaagcttt 1866

ctaggcctga ccctccaggt gtcaatggac ttgtgctact atattttttt attcttggtgta 1926

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tataaactca caaacacaga ttgaaaata atgcacatat ggtgttcaaa ttgaaacctt 2286

tctcatggat ttttgtgggtg tgggccaaata tgggtgtttac attatataat tcctgctgtg 2346

gcaagtaaag cacacttttt ttttctccta aaatgttttt ccctgtgtat cctattatgg 2406

atactggttt tgtaattat gattctttat tttctctcct ttttttagga tatagcagta 2466

atgctattac tgaaatgaat ttcctttttc tgaaatgtaa tcattgatgc ttgaatgata 2526

gaattttagt actgtaaaca ggcttttagtc attaatgtga gagacttaga aaaaaatgct 2586

tagagtggac tattaatatgc gcctaaatga attttgcagt aactggtatt cttggggttt 2646

cctacttaat acacagtaat tcagaacttg tattctatta tgagtttagc agtcttttgg 2706

agtgaccagc aactttgatg tttgcactaa gattttatgt ggaatgcaag agaggttgaa 2766

agaggattca gtagtacaca tacaactaat ttatttgaac tatatgttga agacatctac 2826

cagtttctcc aaatgccttt tttaaaactc atcacagaag attggtgaaa atgctgagta 2886

tgacactttt cttcttgcgt gcatgtcagc tacataaaca gttttgtaca atgaaaatta 2946

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<211> 382

<212> PRT

<213> Homo sapiens

<400> 115

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Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe

20 25 30

Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu

35 40 45

Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val

50 55 60

Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu

65 70 75 80

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val
85 90 95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu
100 105 110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys
115 120 125

Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys
130 135 140

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu
145 150 155 160

Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile
165 170 175

Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
180 185 190

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile
195 200 205

Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn
210 215 220

Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val
225 230 235 240

Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro

245

250

255

Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser

260

265

270

Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu

275

280

285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln

290

295

300

Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met

305

310

315

320

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp

325

330

335

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu

340

345

350

Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser

355

360

365

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile

370

375

380

<210> 116

<211> 3074

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (201)..(1346)

<400> 116

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aacagcagcg gagttttaaa ctttaaatac acaggtctga gtgcctgaac ttgccttttc 120

attttacttc atcctccaag gaggtaaatc acttggcgtg acttcactac ttttaagcaa 180

aagagtgggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233

Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu

1

5

10

gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281

Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser

15

20

25

gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca 329

Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser

30

35

40

gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct 377

Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro
 45 50 55

ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg 425
 Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val
 60 65 70 75

cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg 473
 Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu
 80 85 90

tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac 521
 Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn
 95 100 105

aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg 569
 Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val
 110 115 120

gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att 617
 Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile
 125 130 135

gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac 665
 Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr
 140 145 150 155

atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg 713
 Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu

160	165	170	
atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc			761
Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys			
175	180	185	
aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc			809
Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro			
190	195	200	
acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg			857
Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val			
205	210	215	
tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc			905
Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly			
220	225	230	235
gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt			953
Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser			
240	245	250	
ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat			1001
Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr			
255	260	265	
ttc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct			1049
Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro			
270	275	280	

cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc 1097
 Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg

285 290 295

aat tac aac aag caa gca agt gag caa aac tgg gct aat tac agt gca 1145
 Asn Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala

300 305 310 315

gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat 1193
 Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His

320 325 330

gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta 1241
 Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu

335 340 345

gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct 1289
 Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro

350 355 360

tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac 1337
 Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp

365 370 375

ctg gag atc tagatacagg cttgaaagca tcaagattcc actcaattgt 1386
 Leu Glu Ile

380

ggagaagaaa aaaggtgctg tagaaagtgc accaggtgtt aattttgatc cggtggaggt 1446

ggtactcaac agccttattc atgaggctta gaaaacacaa agacattaga atacctaggt 1506

tcactggggg tgtatggggt agatgggtgg agagggaggg gataagagag gtgcatgttg 1566

gtatttaaag tagtggattc aaagaactta gattataaat aagagttcca ttaggtgata 1626

catagataag ggctttttct ccccgcaaac acccctaaga atggttctgt gtatgtgaat 1686

gagcgggtgg taattgtggc taaatatttt tgttttacca agaaactgaa ataattctgg 1746

ccaggaataa atacttcctg aacatcttag gtcttttcaa caagaaaaag acagaggatt 1806

gtccttaagt ccctgctaaa acattccatt gttaaaattt gcactttgaa ggtaagcttt 1866

ctaggcctga ccctccaggt gtcaatggac ttgtgctact atatTTTTTT attcttggtgta 1926

tcagtttaaa attcagacaa ggcccacaga ataagatttt ccatgcattt gcaaatacgt 1986

atattctttt tccatccact tgcacaatat cattaccatc actttttcat cattcctcag 2046

ctactactca cattcattta atggtttctg taaacatttt taagacagtt gggatgtcac 2106

ttaacatttt ttttttgagc taaagtcagg gaatcaagcc atgcttaata tttaacaatc 2166

acttatatgt gtgtcgaaga gtttgttttg tttgtcatgt attggtacaa gcagatacag 2226

tataaactca caaacacaga ttgaaaata atgcacatat ggtgttcaaa tttgaacctt 2286

tctcatggat ttttgtggtg tgggccaata tgggtgtttac attatataat tcctgctgtg 2346

gcaagtaaag cacacttttt ttttctccta aaatgttttt ccctgtgtat cctattatgg 2406

atactgggtt tgттаattat gattctttat tttctctcct ttttttagga tatagcagta 2466

atgctattac tgaaatgaat ttcctttttc tgaaatgtaa tcattgatgc ttgaatgata 2526

gaattttagt actgtaaaca ggcttttagtc attaatgtga gagacttaga aaaaaatgct 2586

tagagtggac tattaaatgt gcctaaatga attttgcagt aactggtatt cttgggtttt 2646

cctacttaat acacagtaat tcagaacttg tattctatta tgagtttagc agtcttttgg 2706

agtgaccagc aactttgatg tttgcactaa gattttattt ggaatgcaag agaggttgaa 2766

agaggattca gtagtacaca tacaactaat ttatttgaac tatatgttga agacatctac 2826

cagtttctcc aaatgccttt tttaaaactc atcacagaag attggtgaaa atgctgagta 2886

tgacactttt cttcttgcagtc gcatgtcagc tacataaaca gttttgtaca atgaaaatta 2946

ctaatttggt tgacattcca tgttaaacta cggtcatggt cagcttcatt gcatgtaatg 3006

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tttagtat 3074

<210> 117

<211> 398

<212> PRT

<213> Homo sapiens

<400> 117

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met
1 5 10 15

Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu Glu Ala Gly Ala
20 25 30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln
35 40 45

Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser
50 55 60

Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser
65 70 75 80

Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly
85 90 95

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg
100 105 110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn

115	120	125
Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe		
130	135	140
Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala		
145	150	155 160
Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn		
165	170	175
Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val		
180	185	190
Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu		
195	200	205
Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr		
210	215	220
Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala		
225	230	235 240
His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu		
245	250	255
Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr		
260	265	270

Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg
275 280 285

Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro
290 295 300

Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg
305 310 315 320

Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr
325 330 335

Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu
340 345 350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala
355 360 365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile
370 375 380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu
385 390 395

<210> 118

<211> 2054

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76)..(1269)

<400> 118

cacacagctc agaacagctg gatcttgctc agtctctgcc aggggaagat tccttgagg 60

aggccctgca gcgac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc 111

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu

1

5

10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg gga gtg agg gca gag 159

Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu

15

20

25

gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act 207

Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr

30

35

40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255

Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met

45

50

55

60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303

Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys

65

70

75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351

Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu
80 85 90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca 399
Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala
95 100 105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447
Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met
110 115 120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495
Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe
125 130 135 140

ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga 543
Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg
145 150 155

agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc 591
Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr
160 165 170

acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc 639
Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile
175 180 185

ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc 687
Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser

190	195	200	
ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg			735
Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu			
205	210	215	220
acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca			783
Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr			
	225	230	235
caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag			831
Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys			
	240	245	250
gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta			879
Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu			
	255	260	265
gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt			927
Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg			
	270	275	280
gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca			975
Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser			
285	290	295	300
gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa			1023
Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu			
	305	310	315

cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga 1071
 Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly
 320 325 330

gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat 1119
 Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp
 335 340 345

gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag 1167
 Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys
 350 355 360

tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag 1215
 Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu
 365 370 375 380

aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa 1263
 Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln
 385 390 395

gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggcca 1319
 Glu Leu

ggacaaaatg caaacttttt ttttttctga gacagagtct tgctctgtcg ccaagttgca 1379

gtgagccgag atatcgccac tgcaactccag cctgggtgac agagcgagac tccatctcaa 1439

aaaaaaaaa aaaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc 1499

aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt 1559

tggatacagg agaagaaaca gcggctccac tacagacca gccccaggtt caatgtcctc 1619

cgaagaatga agtcctttccc tggatgatgg cccctgccct gtctttccag catccactct 1679

cccttgtcct cctgggggca tatctcagtc aggcagcggc ttcctgatga tggtcgttgg 1739

ggtggttgtc atgtgatggg tcccctccag gttactaaag ggtgcatgtc ccctgcttga 1799

aactgaagg gcaggtggtg agccatggcc atggtcccca gctgaggagc aggtgtccct 1859

gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct 1919

cttaccgggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979

gtcagatct ctagagctgt ctgtgtccccg cccaggattg acctgtgtaa gtcccaataa 2039

actcacctac tcatc 2054

<210> 119

<211> 398

<212> PRT

<213> Homo sapiens

<400> 119

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met

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Ser	Ala	Leu	Phe
Leu	Gly	Val	Arg
Val	Arg	Ala	Glu
Glu	Glu	Ala	Gly
Ala	Gly	Ala	
20	25	30	
Arg	Val	Gln	Gln
Asn	Val	Pro	Ser
Gly	Thr	Asp	Thr
Gly	Asp	Pro	Gln
35	40	45	
Ser	Lys	Pro	Leu
Gly	Asp	Trp	Ala
Ala	Gly	Thr	Met
Asp	Pro	Glu	Ser
50	55	60	
Ser	Ile	Phe	Ile
Glu	Asp	Ala	Ile
Lys	Tyr	Phe	Lys
Glu	Lys	Val	Ser
65	70	75	80
Thr	Gln	Asn	Leu
Leu	Leu	Leu	Leu
Thr	Asp	Asn	Glu
Ala	Trp	Asn	Gly
85	90	95	
Phe	Val	Ala	Ala
Ala	Glu	Leu	Pro
Arg	Asn	Glu	Ala
Asp	Glu	Leu	Arg
100	105	110	
Lys	Ala	Leu	Asp
Asn	Leu	Ala	Arg
Gln	Met	Ile	Met
Lys	Asp	Lys	Asn
115	120	125	
Trp	His	Asp	Lys
Gly	Gln	Gln	Tyr
Arg	Asn	Trp	Phe
Leu	Lys	Glu	Phe
130	135	140	
Pro	Arg	Leu	Lys
Ser	Lys	Leu	Glu
Asp	Asn	Ile	Arg
Arg	Leu	Arg	Ala
145	150	155	160

Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn
165 170 175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val
180 185 190

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu
195 200 205

Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr
210 215 220

Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala
225 230 235 240

His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu
245 250 255

Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr
260 265 270

Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg
275 280 285

Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro
290 295 300

Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg
305 310 315 320

Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr
325 330 335

Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu
340 345 350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala
355 360 365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile
370 375 380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu
385 390 395

<210> 120

<211> 2054

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76)..(1269)

<400> 120

cacacagctc agaacagctg gatcttgctc agtctctgcc aggggaagat tccttgagg 60

aggccctgca gcgac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc 111

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu

1

5

10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg aga gtg agg gca gag 159

Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu

15

20

25

gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act 207

Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr

30

35

40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg 255

Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met

45

50

55

60

gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag 303

Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys

65

70

75

gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag 351

Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu

80

85

90

gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca 399

Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala

95

100

105

gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg 447

Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met
110 115 120

aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt 495
Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe
125 130 135 140

ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga 543
Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg
145 150 155

agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc 591
Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr
160 165 170

acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc 639
Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile
175 180 185

ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc 687
Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser
190 195 200

ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg 735
Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu
205 210 215 220

acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca 783
Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr

225	230	235	
caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag	831		
Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys			
240	245	250	
gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta	879		
Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu			
255	260	265	
gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt	927		
Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg			
270	275	280	
gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca	975		
Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser			
285	290	295	300
gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa	1023		
Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu			
305	310	315	
cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga	1071		
Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly			
320	325	330	
gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat	1119		
Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp			
335	340	345	

gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag 1167

Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys

350

355

360

tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag 1215

Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu

365

370

375

380

aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa 1263

Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln

385

390

395

gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggccca 1319

Glu Leu

ggacaaaatg caaacttttt ttttttctga gacagagtct tgctctgtcg ccaagttgca 1379

gtgagccgag atatcgccac tgcactccag cctgggtgac agagcgagac tccatctcaa 1439

aaaaaaaaa aaaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc 1499

aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt 1559

tggatacagg agaagaaaca gcggctccac tacagacca gccccaggtt caatgtcctc 1619

cgaagaatga agtctttccc tggatgatggt cccctgccct gtctttccag catccactct 1679

cccttgtcct cctgggggca tatctcagtc aggcagcggc ttctgatga tggtcgttgg 1739

ggtggttgtc atgtgatggg tccccccag gttactaaag ggtgcatgtc ccctgcttga 1799

acactgaagg gcaggtgggtg agccatggcc atgggtcccca gctgaggagc aggtgtccct 1859

gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct 1919

cttaccgggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979

gctcagatct ctagagctgt cttgtccccg cccaggattg acctgtgtaa gtcccaataa 2039

actcacctac tcatac 2054

<210> 121

<211> 108

<212> PRT

<213> Homo sapiens

<400> 121

Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe

1 5 10 15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu

20 25 30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys

35 40 45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val
50 55 60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp
65 70 75 80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala
85 90 95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu
100 105

<210> 122

<211> 1546

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (89)..(412)

<400> 122

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gcccgcccgc tcagcgtccg ccgccgcc atg gga gtg cag gtg gaa acc atc 112

Met Gly Val Gln Val Glu Thr Ile

1

5

tcc cca gga gac ggg cgc acc ttc ccc aag cgc ggc cag acc tgc gtg 160
 Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val
 10 15 20

gtg cac tac acc ggg atg ctt gaa gat gga aag aaa ttt gat tcc tcc 208
 Val His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser
 25 30 35 40

cgg gac aga aac aag ccc ttt aag ttt atg cta ggc aag cag gag gtg 256
 Arg Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val
 45 50 55

atc cga ggc tgg gaa gaa ggg gtt gcc cag atg agt gtg ggt cag aga 304
 Ile Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg
 60 65 70

gcc aaa ctg act ata tct cca gat tat gcc tat ggt gcc act ggg cac 352
 Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His
 75 80 85

cca ggc atc atc cca cca cat gcc act ctc gtc ttc gat gtg gag ctt 400
 Pro Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu
 90 95 100

cta aaa ctg gaa tgacaggaat ggcctcctcc cttagctccc tggttcttgga 452
 Leu Lys Leu Glu
 105

tctgccatgg agggatctgg tgcctccaga catgtgcaca tgaatccata tggagctttt 512

cctgatgttc cactccactt tgtatagaca tctgccctga ctgaatgtgt tctgtcactc 572

agctttgctt ccgacacctc tgtttcctct tcccctttct cctcgtatgt gtgtttacct 632

aaactatatg ccataaacct caagttactc attttatttt gttttcattt tgggggtgaag 692

attcagtttc agtccttttg atataggttt ccaattaagt acatgggtcaa gtattaacag 752

cacaagtggg aggttaacat tagaatagga attggtgttg gggggggggg ttgcaagaat 812

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tgcgctgcaa agccatagca gatttgaggc gctgttgagg actgaattac tctccaagtt 932

gagagatgtc ttggggttaa attaaaagcc ctacctaaaa ctgaggtggg gatggggaga 992

gcctttgcct ccaccattcc caccacccct ccccttaaac cctctgcctt tgaaagtaga 1052

tcatgttcac tgcaatgctg gacactacag gtatctgtcc ctgggccagc aggacctct 1112

gaagccttct ttgtggcctt tttttttttt tcatcctgtg gtttttctaa tggactttca 1172

ggaattttgt aatctcataa ctttccaagc tccaccactt cctaaatctt aagaacttta 1232

attgacagtt tcaattgaag gtgctgtttg tagacttaac acccagtgaag agcccagcca 1292

tcatgacaaa tccttgaatg ttctcttaag aaaatgatgc tggtcacgc agcttcagca 1352

tctcctgttt tttgatgctt ggctccctct gctgatctca gtttcctggc ttttcctccc 1412

tcagccctt ctcacccctt tgctgtcctg tgtagtgatt tggtagagaaa tcgttgctgc 1472

acccttcccc cagcaccatt tatgagtctc aagttttatt attgcaataa aagtgcctta 1532

tgccggttt tctc 1546

<210> 123

<211> 679

<212> PRT

<213> Homo sapiens

<400> 123

Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala Thr Ala Ala Ser Gly

1 5 10 15

Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu Gly Phe Ile Ile Ala

20 25 30

Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp Val Ala Asn Ser Phe

35 40 45

Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu Lys Gln Ala Cys Ile

50 55 60

Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val Leu Leu Gly Ala Lys

65 70 75 80

Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp Val Glu Met Tyr Asn
85 90 95

Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val Ser Ala Met Phe Gly
100 105 110

Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu Lys Leu Pro Ile Ser
115 120 125

Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly Phe Ser Leu Val Ala
130 135 140

Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu Ile Lys Ile Val Met
145 150 155 160

Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile Met Ser Gly Ile Leu
165 170 175

Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys Ala Asp Pro Val Pro
180 185 190

Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala Cys Thr Val Gly Ile
195 200 205

Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro Leu Leu Gly Phe Asp
210 215 220

Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser Val Gly Cys Ala Val

225 230 235 240

Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys Pro Arg Met Lys Arg
245 250 255

Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser Glu Ser Pro Leu Met
260 265 270

Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu Glu Thr Lys Leu Ser
275 280 285

Val Gly Asp Ile Glu Asn Lys His Pro Val Ser Glu Val Gly Pro Ala
290 295 300

Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg Thr Val Ser Phe Lys
305 310 315 320

Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu Arg Leu Pro Ser Val
325 330 335

Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr Val Asn Gly Ala Val
340 345 350

Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser Gln Ala Val Ser Asn
355 360 365

Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His Thr Val His Lys Asp
370 375 380

Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu His Leu Ala Lys Val
385 390 395 400

Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro Leu Arg Arg Asn Asn
405 410 415

Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly Met Pro Leu Asp Ser
420 425 430

Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu Glu Met Glu Lys Leu
435 440 445

Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile Arg Met Asp Ser Tyr
450 455 460

Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His Ser Ala Ser Glu Ile
465 470 475 480

Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly Asp Arg Lys Gly Ser
485 490 495

Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp Lys Pro Glu Val Ser
500 505 510

Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala Cys Phe Gly Ser Phe
515 520 525

Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile Gly Pro Leu Val Ala
530 535 540

Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser Ser Lys Val Ala Thr
545 550 555 560

Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly Ile Cys Val Gly Leu
565 570 575

Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met Gly Lys Asp Leu Thr
580 585 590

Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu Leu Ala Ser Ala Leu
595 600 605

Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro Ile Ser Thr Thr His
610 615 620

Cys Lys Val Gly Ser Val Val Ser Val Gly Trp Leu Arg Ser Lys Lys
625 630 635 640

Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe Met Ala Trp Phe Val
645 650 655

Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala Ile Met Ala Ile Phe
660 665 670

Arg Tyr Val Ile Leu Arg Met
675

<210> 124

<211> 2916

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (81)..(2117)

<400> 124

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aacaaccact actccagaga atg gca acg ctg att acc agt act aca gct gct 113

Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala

1

5

10

acc gcc gct tct ggt cct ttg gtg gac tac cta tgg atg ctc atc ctg 161

Thr Ala Ala Ser Gly Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu

15

20

25

ggc ttc att att gca ttt gtc ttg gca ttc tcc gtg gga gcc aat gat 209

Gly Phe Ile Ile Ala Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp

30

35

40

gta gca aat tct ttt ggt aca gct gtg ggc tca ggt gta gtg acc ctg 257

Val Ala Asn Ser Phe Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu

45

50

55

aag caa gcc tgc atc cta gct agc atc ttt gaa aca gtg ggc tct gtc 305

Lys Gln Ala Cys Ile Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val
60 65 70 75

tta ctg ggg gcc aaa gtg agc gaa acc atc cgg aag ggc ttg att gac 353
Leu Leu Gly Ala Lys Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp
80 85 90

gtg gag atg tac aac tcg act caa ggg ctg ctg atg gcc ggc tca gtc 401
Val Glu Met Tyr Asn Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val
95 100 105

agt gct atg ttt ggt tct gct gtg tgg caa ctc gtg gct tcg ttt ttg 449
Ser Ala Met Phe Gly Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu
110 115 120

aag ctc cct att tct gga acc cat tgt att gtt ggt gca act att ggt 497
Lys Leu Pro Ile Ser Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly
125 130 135

ttc tcc ctc gtg gca aag ggg cag gag ggt gtc aag tgg tct gaa ctg 545
Phe Ser Leu Val Ala Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu
140 145 150 155

ata aaa att gtg atg tct tgg ttc gtg tcc cca ctg ctt tct gga att 593
Ile Lys Ile Val Met Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile
160 165 170

atg tct gga att tta ttc ttc ctg gtt cgt gca ttc atc ctc cat aag 641
Met Ser Gly Ile Leu Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys

175	180	185	
gca gat cca gtt cct aat ggt ttg cga gct ttg cca gtt ttc tat gcc	689		
Ala Asp Pro Val Pro Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala			
190	195	200	
tgcaaca gtt gga ata aac ctc ttt tcc atc atg tat act gga gca ccg	737		
Cys Thr Val Gly Ile Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro			
205	210	215	
ttg ctg ggc ttt gac aaa ctt cct ctg tgg ggt acc atc ctc atc tcg	785		
Leu Leu Gly Phe Asp Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser			
220	225	230	235
gtg gga tgt gca gtt ttc tgt gcc ctt atc gtc tgg ttc ttt gta tgt	833		
Val Gly Cys Ala Val Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys			
240	245	250	
ccc agg atg aag aga aaa att gaa cga gaa ata aag tgt agt cct tct	881		
Pro Arg Met Lys Arg Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser			
255	260	265	
gaa agc ccc tta atg gaa aaa aag aat agc ttg aaa gaa gac cat gaa	929		
Glu Ser Pro Leu Met Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu			
270	275	280	
gaa aca aag ttg tct gtt ggt gat att gaa aac aag cat cct gtt tct	977		
Glu Thr Lys Leu Ser Val Gly Asp Ile Glu Asn Lys His Pro Val Ser			
285	290	295	

gag gta ggg cct gcc act gtg ccc ctc cag gct gtg gtg gag gag aga 1025
 Glu Val Gly Pro Ala Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg
 300 305 310 315

aca gtc tca ttc aaa ctt gga gat ttg gag gaa gct cca gag aga gag 1073
 Thr Val Ser Phe Lys Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu
 320 325 330

agg ctt ccc agc gtg gac ttg aaa gag gaa acc agc ata gat agc acc 1121
 Arg Leu Pro Ser Val Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr
 335 340 345

gtg aat ggt gca gtg cag ttg cct aat ggg aac ctt gtc cag ttc agt 1169
 Val Asn Gly Ala Val Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser
 350 355 360

caa gcc gtc agc aac caa ata aac tcc agt ggc cac tac cag tat cac 1217
 Gln Ala Val Ser Asn Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His
 365 370 375

acc gtg cat aag gat tcc ggc ctg tac aaa gag cta ctc cat aaa tta 1265
 Thr Val His Lys Asp Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu
 380 385 390 395

cat ctt gcc aag gtg gga gat tgc atg gga gac tcc ggt gac aaa ccc 1313
 His Leu Ala Lys Val Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro
 400 405 410

tta agg cgc aat aat agc tat act tcc tat acc atg gca ata tgt ggc 1361
 Leu Arg Arg Asn Asn Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly
 415 420 425

atg cct ctg gat tca ttc cgt gcc aaa gaa ggt gaa cag aag ggc gaa 1409
 Met Pro Leu Asp Ser Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu
 430 435 440

gaa atg gag aag ctg aca tgg cct aat gca gac tcc aag aag cga att 1457
 Glu Met Glu Lys Leu Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile
 445 450 455

cga atg gac agt tac acc agt tac tgc aat gct gtg tct gac ctt cac 1505
 Arg Met Asp Ser Tyr Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His
 460 465 470 475

tca gca tct gag ata gac atg agt gtc aag gca gag atg ggt cta ggt 1553
 Ser Ala Ser Glu Ile Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly
 480 485 490

gac aga aaa gga agt aat ggc tct cta gaa gaa tgg tat gac cag gat 1601
 Asp Arg Lys Gly Ser Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp
 495 500 505

aag cct gaa gtc tct ctc ctc ttc cag ttc ctg cag atc ctt aca gcc 1649
 Lys Pro Glu Val Ser Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala
 510 515 520

tgc ttt ggg tca ttc gcc cat ggt ggc aat gac gta agc aat gcc att 1697
 441/754

Cys Phe Gly Ser Phe Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile

525

530

535

ggg cct ctg gtt gct tta tat ttg gtt tat gac aca gga gat gtt tct 1745

Gly Pro Leu Val Ala Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser

540

545

550

555

tca aaa gtg gca aca cca ata tgg ctt cta ctc tat ggt ggt gtt ggt 1793

Ser Lys Val Ala Thr Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly

560

565

570

atc tgt gtt ggt ctg tgg gtt tgg gga aga aga gtt atc cag acc atg 1841

Ile Cys Val Gly Leu Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met

575

580

585

ggg aag gat ctg aca ccg atc aca ccc tct agt ggc ttc agt att gaa 1889

Gly Lys Asp Leu Thr Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu

590

595

600

ctg gca tct gcc ctc act gtg gtg att gca tca aat att ggc ctt ccc 1937

Leu Ala Ser Ala Leu Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro

605

610

615

atc agt aca aca cat tgt aaa gtg ggc tct gtt gtg tct gtt ggc tgg 1985

Ile Ser Thr Thr His Cys Lys Val Gly Ser Val Val Ser Val Gly Trp

620

625

630

635

ctc cgg tcc aag aag gct gtt gac tgg cgt ctc ttt cgt aac att ttt 2033

Leu Arg Ser Lys Lys Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe

640

645

650

atg gcc tgg ttt gtc aca gtc cct att tct gga gtt atc agt gct gcc 2081

Met Ala Trp Phe Val Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala

655

660

665

atc atg gca atc ttc aga tat gtc atc ctc aga atg tgaagctgtt 2127

Ile Met Ala Ile Phe Arg Tyr Val Ile Leu Arg Met

670

675

tgagattaaa atttgtgtca atgtttggga ccattcttagg tattcctgct ccctgaaga 2187

atgattacag tgtaacaga agactgacaa gagtcttttt atttgggagc cagaggaggg 2247

aagtgttact tgtgctataa ctgcttttgt gctaaatatg aattgtctca aaattagctg 2307

tgtaaaatag cccgggttcc actggctcct gctgaggtcc ctttccttc tgggctgtga 2367

attcctgtac atatttctct actttttgta tcaggcttca attccattat gttttaatgt 2427

tgtctctgaa gatgacttgt gatttttttt tctttttttt aaaccatgaa gagccgtttg 2487

acagagcatg ctctgcgttg ttggtttcac cagcttctgc cctcacatgc acagggattt 2547

aacaacaaaa atataactac aacttccctt gtagtctctt atataagtag agtccttggt 2607

actctgccct cctgtcagta gtggcaggat ctattggcat attcgggagc ttcttagagg 2667

gatgaggttc ttggaacaca gtgaaaattt aaattagtaa cttttttgca agcagtttat 2727

tgactgttat tgctaagaag aagtaagaaa gaaaaagcct gttggcaatc ttggttattt 2787

ctttaagatt tctggcagtg tgggatggat gaatgaagtg gaatgtgaac tttgggcaag 2847

ttaaattggga cagccttcca tgttcatttg tctacctctt aactgaataa aaaagcctac 2907

agtttttag 2916

<210> 125

<211> 288

<212> PRT

<213> Homo sapiens

<400> 125

Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln Asp Leu Ser Glu Ala

1 5 10 15

Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln Ala Glu Asn Ala Glu

20 25 30

Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr Arg Asp Gly Phe Lys

35 40 45

Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val Ala Leu Glu Glu Glu

50 55 60

Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala Pro Val Tyr Phe Pro

65		70		75		80									
Glu	Glu	Leu	His	Arg	Lys	Ala	Ala	Leu	Glu	Gln	Asp	Leu	Ala	Phe	Trp
				85					90					95	
Tyr	Gly	Pro	Arg	Trp	Gln	Glu	Val	Ile	Pro	Tyr	Thr	Pro	Ala	Met	Gln
				100					105					110	
Arg	Tyr	Val	Lys	Arg	Leu	His	Glu	Val	Gly	Arg	Thr	Glu	Pro	Glu	Leu
				115					120					125	
Leu	Val	Ala	His	Ala	Tyr	Thr	Arg	Tyr	Leu	Gly	Asp	Leu	Ser	Gly	Gly
				130					135					140	
Gln	Val	Leu	Lys	Lys	Ile	Ala	Gln	Lys	Ala	Leu	Asp	Leu	Pro	Ser	Ser
				145					150					155	
Gly	Glu	Gly	Leu	Ala	Phe	Phe	Thr	Phe	Pro	Asn	Ile	Ala	Ser	Ala	Thr
				165					170					175	
Lys	Phe	Lys	Gln	Leu	Tyr	Arg	Ser	Arg	Met	Asn	Ser	Leu	Glu	Met	Thr
				180					185					190	
Pro	Ala	Val	Arg	Gln	Arg	Val	Ile	Glu	Glu	Ala	Lys	Thr	Ala	Phe	Leu
				195					200					205	
Leu	Asn	Ile	Gln	Leu	Phe	Glu	Glu	Leu	Gln	Glu	Leu	Leu	Thr	His	Asp
				210					215					220	

Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly Leu Arg Gln Arg Ala
 225 230 235 240

Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu Thr Pro Arg Gly Lys
 245 250 255

Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu Leu Arg Trp Val Leu
 260 265 270

Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val Gly Leu Tyr Ala Met
 275 280 285

<210> 126

<211> 1550

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (81).. (944)

<400> 126

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acgagcccag caccggccgg atg gag cgt ccg caa ccc gac agc atg ccc cag 113

Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln

1

5

10

gat ttg tca gag gcc ctg aag gag gcc acc aag gag gtg cac acc cag 161
 Asp Leu Ser Glu Ala Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln
 15 20 25

gca gag aat gct gag ttc atg agg aac ttt cag aag ggc cag gtg acc 209
 Ala Glu Asn Ala Glu Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr
 30 35 40

cga gac ggc ttc aag ctg gtg atg gcc tcc ctg tac cac atc tat gtg 257
 Arg Asp Gly Phe Lys Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val
 45 50 55

gcc ctg gag gag gag att gag cgc aac aag gag agc cca gtc ttc gcc 305
 Ala Leu Glu Glu Glu Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala
 60 65 70 75

cct gtc tac ttc cca gaa gag ctg cac cgc aag gct gcc ctg gag cag 353
 Pro Val Tyr Phe Pro Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln
 80 85 90

gac ctg gcc ttc tgg tac ggg ccc cgc tgg cag gag gtc atc ccc tac 401
 Asp Leu Ala Phe Trp Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr
 95 100 105

aca cca gcc atg cag cgc tat gtg aag cgg ctc cac gag gtg ggg cgc 449
 Thr Pro Ala Met Gln Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg
 110 115 120

aca gag ccc gag ctg ctg gtg gcc cac gcc tac acc cgc tac ctg ggt 497

Thr Glu Pro Glu Leu Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly
125 130 135

gac ctg tct ggg ggc cag gtg ctc aaa aag att gcc cag aaa gcc ctg 545
Asp Leu Ser Gly Gly Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu
140 145 150 155

gac ctg ccc agc tct ggc gag ggc ctg gcc ttc ttc acc ttc ccc aac 593
Asp Leu Pro Ser Ser Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn
160 165 170

att gcc agt gcc acc aag ttc aag cag ctc tac cgc tcc cgc atg aac 641
Ile Ala Ser Ala Thr Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn
175 180 185

tcc ctg gag atg act ccc gca gtc agg cag agg gtg ata gaa gag gcc 689
Ser Leu Glu Met Thr Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala
190 195 200

aag act gcg ttc ctg ctc aac atc cag ctc ttt gag gag ttg cag gag 737
Lys Thr Ala Phe Leu Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu
205 210 215

ctg ctg acc cat gac acc aag gac cag agc ccc tca cgg gca cca ggg 785
Leu Leu Thr His Asp Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly
220 225 230 235

ctt cgc cag cgg gcc agc aac aaa gtg caa gat tct gcc ccc gtg gag 833
Leu Arg Gln Arg Ala Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu

240

245

250

act ccc aga ggg aag ccc cca ctc aac acc cgc tcc cag gct ccg ctt 881

Thr Pro Arg Gly Lys Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu

255

260

265

ctc cga tgg gtc ctt aca ctc agc ttt ctg gtg gcg aca gtt gct gta 929

Leu Arg Trp Val Leu Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val

270

275

280

ggg ctt tat gcc atg tgaatgcagg catgctggct cccagggcca tgaactttgt 984

Gly Leu Tyr Ala Met

285

ccggtggaag gccttccttc tagagaggga attctcttgg ctggcttcct taccgtgggc 1044

actgaaggct ttcagggcct ccagccctct cactgtgtcc ctctctctgg aaaggaggaa 1104

ggagcctatg gcctcttccc caacgaaaag cacatccagg caatggccta aacttcagag 1164

ggggcgaagg ggtcagccct gcccttcagc atcctcagtt cctgcagcag agcctggaag 1224

acacccta atgtgcagctg tctcaaacct ccaaaagccc tgagtttcaa gtatccttgt 1284

tgacacggcc atgaccactt tccccgtggg ccatggcaat ttttacacaa acctgaaaag 1344

atgttgtgtc ttgtgttttt gtcttatttt tgttggagcc actctgttcc tggtcagcc 1404

tcaaatgcag tatttttgtt gtgttctgtt gtttttatag cagggttggg gtggtttttg 1464

agccatgcgt gggtagggag ggaggtgttt aacggcactg tggccttggt ctaacttttg 1524

tgtgaaataa taaacaacat tgtctg 1550

<210> 127

<211> 135

<212> PRT

<213> Homo sapiens

<400> 127

Met Ala Cys Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu

1 5 10 15

Cys Leu Arg Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val

20 25 30

Leu Asn Leu Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro

35 40 45

Arg Phe Asn Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys

50 55 60

Asp Gly Gly Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe

65 70 75 80

Gln Pro Gly Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn

85 90 95

Leu Thr Val Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg

100

105

110

Leu Asn Leu Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys

115

120

125

Ile Lys Cys Val Ala Phe Asp

130

135

<210> 128

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)..(454)

<400> 128

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Met Ala Cys

1

ggt ctg gtc gcc agc aac ctg aat ctc aaa cct gga gag tgc ctt cga 106

Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu Cys Leu Arg

5

10

15

gtg cga ggc gag gtg gct cct gac gct aag agc ttc gtg ctg aac ctg 154
Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val Leu Asn Leu
20 25 30 35

ggc aaa gac agc aac aac ctg tgc ctg cac ttc aac cct cgc ttc aac 202
Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro Arg Phe Asn
40 45 50

gcc cac ggc gac gcc aac acc atc gtg tgc aac agc aag gac ggc ggg 250
Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys Asp Gly Gly
55 60 65

gcc tgg ggg acc gag cag cgg gag gct gtc ttt ccc ttc cag cct gga 298
Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe Gln Pro Gly
70 75 80

agt gtt gca gag gtg tgc atc acc ttc gac cag gcc aac ctg acc gtc 346
Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn Leu Thr Val
85 90 95

aag ctg cca gat gga tac gaa ttc aag ttc ccc aac cgc ctc aac ctg 394
Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg Leu Asn Leu
100 105 110 115

gag gcc atc aac tac atg gca gct gac ggt gac ttc aag atc aaa tgt 442
Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys Ile Lys Cys
120 125 130

gtg gcc ttt gac tgaaatcagc cagcccatgg cccccaataa aggcagctgc 494

Val Ala Phe Asp

135

ctctgctccc ctg

507

<210> 129

<211> 662

<212> PRT

<213> Homo sapiens

<400> 129

Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn

1

5

10

15

Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn

20

25

30

Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp

35

40

45

Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys

50

55

60

Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser

65

70

75

80

Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr

85

90

95

Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu
100 105 110

Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys
115 120 125

His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile
130 135 140

Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu
145 150 155 160

Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro
165 170 175

Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg
180 185 190

Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr
195 200 205

Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu
210 215 220

Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu
225 230 235 240

Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu

245	250	255
Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr		
260	265	270
Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln		
275	280	285
Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys		
290	295	300
Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val		
305	310	315
Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala		
325	330	335
Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe		
340	345	350
Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp		
355	360	365
Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln		
370	375	380
Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp		
385	390	395
		400

Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu
405 410 415

Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe
420 425 430

Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn
435 440 445

Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile
450 455 460

Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp
465 470 475 480

Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu
485 490 495

Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser
500 505 510

Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr
515 520 525

Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn
530 535 540

Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly
545 550 555 560

Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln

565 570 575

Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln

580 585 590

Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn

595 600 605

Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe

610 615 620

Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn

625 630 635 640

Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg

645 650 655

Leu Arg Ile Ser Glu Lys

660

<210> 130

<211> 2251

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74).. (2059)

<400> 130

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tcagtggttc aaa atg aat aaa gag att cca aat gga aat aca tca gag 109

Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu

1 5 10

ctt att ttt aat gca gtg cat gta aaa gat gca ggc ttt tat gtc tgt 157

Leu Ile Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys

15 20 25

cga gtt aat aac aat ttc acc ttt gaa ttc agc cag tgg tca cag ctg 205

Arg Val Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu

30 35 40

gat gtt tgc gac atc cca gag agc ttc cag aga agt gtt gat ggc gtc 253

Asp Val Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val

45 50 55 60

tct gaa tcc aag ttg caa atc tgt gtt gaa cca act tcc caa aag ctg 301

Ser Glu Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu

65 70 75

atg cca ggc agc aca ttg gtt tta cag tgt gtt gct gtt gga agc cct 349

Met Pro Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro

80 85 90

att cct cac tac cag tgg ttc aaa aat gaa tta cca tta aca cat gag 397

Ile Pro His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu

95

100

105

acc aaa aag cta tac atg gtg cct tat gtg gat ttg gaa cac caa gga 445

Thr Lys Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly

110

115

120

acc tac tgg tgt cat gta tat aat gat cga gac agt caa gat agc aag 493

Thr Tyr Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys

125

130

135

140

aag gta gaa atc atc ata gga aga aca gat gag gca gtg gag tgc act 541

Lys Val Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr

145

150

155

gaa gat gaa tta aat aat ctt ggt cat cct gat aat aaa gag caa aca 589

Glu Asp Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr

160

165

170

act gac cag cct ttg gcg aag gac aag gtt gcc ctt ttg ata gga aat 637

Thr Asp Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn

175

180

185

atg aat tac cgg gag cac ccc aag ctc aaa gct cct ttg gtg gat gtg 685

Met Asn Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val

190

195

200

tac gaa ttg act aac tta ctg aga cag ctg gac ttc aaa gtg gtt tca 733
Tyr Glu Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser
205 210 215 220

ctg ttg gat ctt act gaa tat gag atg cgt aat gct gtg gat gag ttt 781
Leu Leu Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe
225 230 235

tta ctc ctt tta gac aag gga gta tat ggg tta tta tat tat gca gga 829
Leu Leu Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly
240 245 250

cat ggt tat gaa aat ttt ggg aac agc ttc atg gtc ccc gtt gat gct 877
His Gly Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala
255 260 265

cca aat cca tat agg tct gaa aat tgt ctg tgt gta caa aat ata ctg 925
Pro Asn Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu
270 275 280

aaa ttg atg caa gaa aaa gaa act gga ctt aat gtg ttc tta ttg gat 973
Lys Leu Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp
285 290 295 300

atg tgt agg aaa aga aat gac tac gat gat acc att cca atc ttg gat 1021
Met Cys Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp
305 310 315

gca cta aaa gtc acc gcc aat att gtg ttt gga tat gcc acg tgt caa 1069

Ala Leu Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln

320

325

330

gga gca gaa gct ttt gaa atc cag cat tct gga ttg gca aat gga atc 1117

Gly Ala Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile

335

340

345

ttt atg aaa ttt tta aaa gac aga tta tta gaa gat aag aaa atc act 1165

Phe Met Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr

350

355

360

gtg tta ctg gat gaa gtt gca gaa gat atg ggt aag tgt cac ctt acc 1213

Val Leu Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr

365

370

375

380

aaa ggc aaa cag gct cta gag att cga agt agt tta tct gag aag aga 1261

Lys Gly Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg

385

390

395

gca ctt act gat cca ata cag gga aca gaa tat tct gct gaa tct ctt 1309

Ala Leu Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu

400

405

410

gtg cgg aat cta cag tgg gcc aag gct cat gaa ctt cca gaa agt atg 1357

Val Arg Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met

415

420

425

tgt ctt aag ttt gac tgt ggt gtt cag att caa tta gga ttt gca gct 1405

Cys Leu Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala

430	435	440	
gag ttt tcc aat gtc atg atc atc tat aca agt ata gtt tac aaa cca 1453			
Glu Phe Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro			
445	450	455	460
ccg gag ata ata atg tgt gat gcc tac gtt act gat ttt cca ctt gat 1501			
Pro Glu Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp			
	465	470	475
cta gat att gat cca aaa gat gca aat aaa ggc aca cct gaa gaa act 1549			
Leu Asp Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr			
	480	485	490
ggc agc tac ttg gta tca aag gat ctt ccc aag cat tgc ctc tat acc 1597			
Gly Ser Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr			
	495	500	505
aga ctc agt tca ctg caa aaa tta aag gaa cat cta gtc ttc aca gta 1645			
Arg Leu Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val			
	510	515	520
tgt tta tca tat cag tac tca gga ttg gaa gat act gta gag gac aag 1693			
Cys Leu Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys			
525	530	535	540
cag gaa gtg aat gtt ggg aaa cct ctc att gct aaa tta gac atg cat 1741			
Gln Glu Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His			
	545	550	555

cga ggt ttg gga agg aag act tgc ttt caa act tgt ctt atg tct aat 1789
 Arg Gly Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn

560 565 570

ggt cct tac cag agt tct gca gcc acc tca gga gga gca ggg cat tat 1837
 Gly Pro Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr

575 580 585

cac tca ttg caa gac cca ttc cat ggt gtt tac cat tca cat cct ggt 1885
 His Ser Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly

590 595 600

aat cca agt aat gtt aca cca gca gat agc tgt cat tgc agc cgg act 1933
 Asn Pro Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr

605 610 615 620

cca gat gca ttt att tca agt ttc gct cac cat gct tca tgt cat ttt 1981
 Pro Asp Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe

625 630 635

agt aga agt aat gtg cca gta gag aca act gat gaa ata cca ttt agt 2029
 Ser Arg Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser

640 645 650

ttc tct gac agg ctc aga att tct gaa aaa tgacctcctt gtttttgaaa 2079
 Phe Ser Asp Arg Leu Arg Ile Ser Glu Lys

655 660

gtagcataa ttttagatgc ctgtgaaata gtactgcact tacataaagt gagacattgt 2139

gaaaaggcaa atttgtatat gtagagaaag aatagtagta actgtttcat agcaaacttc 2199

aggactttga gatgttgaaa ttacattatt taattacaga cttcctcttt ct 2251

<210> 131

<211> 824

<212> PRT

<213> Homo sapiens

<400> 131

Met Ser Leu Leu Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala

1 5 10 15

Pro Thr Gly Pro Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg

20 25 30

Leu Arg Glu Pro Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala

35 40 45

Pro Glu Gly Arg Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg

50 55 60

Gly Arg Leu Arg Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys

65 70 75 80

Val Leu Glu Pro Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met

	85	90	95
Gly Glu Lys Gly Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala			
	100	105	110
Met Glu His Thr Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys			
	115	120	125
Ile Thr Val Asn Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val			
	130	135	140
Lys Leu Cys Cys Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp			
	145	150	155
			160
Phe Lys Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile			
	165	170	175
Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val			
	180	185	190
Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val			
	195	200	205
Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu			
	210	215	220
Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro			
	225	230	235
			240

Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro
245 250 255

His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys
260 265 270

Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr
275 280 285

Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val
290 295 300

Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp
305 310 315 320

Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp
325 330 335

Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn
340 345 350

Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu
355 360 365

Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu
370 375 380

Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu
385 390 395 400

Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly
405 410 415

Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn
420 425 430

Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu
435 440 445

Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys
450 455 460

Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu
465 470 475 480

Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala
485 490 495

Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met
500 505 510

Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu
515 520 525

Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly
530 535 540

Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu
467/754

545 550 555 560

Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg
565 570 575

Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu
580 585 590

Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe
595 600 605

Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu
610 615 620

Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp
625 630 635 640

Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser
645 650 655

Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu
660 665 670

Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu
675 680 685

Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu
690 695 700

Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly
705 710 715 720

Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro
725 730 735

Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser
740 745 750

Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro
755 760 765

Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp
770 775 780

Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg
785 790 795 800

Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser
805 810 815

Asp Arg Leu Arg Ile Ser Glu Lys
820

<210> 132

<211> 2828

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (165).. (2636)

<400> 132

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gcccctgcct ccgcggctcg gaggcgagcg gaagggtccc cggggccgag gcccgtgacg 120

gggcgggcgg gagccccggc agtccgggggt cgccggcgag ggcc atg tcg ctg ttg 176

Met Ser Leu Leu

1

ggg gac ccg cta cag gcc ctg ccg ccc tcg gcc gcc ccc acg ggg ccg 224

Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala Pro Thr Gly Pro

5

10

15

20

ctg ctc gcc cct ccg gcc ggc gcg acc ctc aac cgc ctg cgg gag ccg 272

Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg Leu Arg Glu Pro

25

30

35

ctg ctg cgg agg ctc agc gag ctc ctg gat cag gcg ccc gag ggc cgg 320

Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala Pro Glu Gly Arg

40

45

50

ggc tgg agg aga ctg gcg gag ctg gcg ggg agt cgc ggg cgc ctc cgc 368

Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg Gly Arg Leu Arg

55

60

65

ctc agt tgc cta gac ctg gag cag tgt tct ctt aag gta ctg gag cct 416

Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys Val Leu Glu Pro

70

75

80

gaa gga agc ccc agc ctg tgt ctg ctg aag tta atg ggt gaa aaa ggt 464

Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met Gly Glu Lys Gly

85

90

95

100

tgc aca gtc aca gaa ttg agt gat ttc ctg cag gct atg gaa cac act 512

Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala Met Glu His Thr

105

110

115

gaa gtt ctt cag ctt ctc agc ccc cca gga ata aag att act gta aac 560

Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys Ile Thr Val Asn

120

125

130

cca gag tca aag gca gtc ttg gct gga cag ttt gtg aaa ctg tgt tgc 608

Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val Lys Leu Cys Cys

135

140

145

cgg gca act gga cat cct ttt gtt caa tat cag tgg ttc aaa atg aat 656

Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp Phe Lys Met Asn

150

155

160

aaa gag att cca aat gga aat aca tca gag ctt att ttt aat gca gtg 704

Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn Ala Val

165

170

175

180

cat gta aaa gat gca ggc ttt tat gtc tgt cga gtt aat aac aat ttc	752
His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn Asn Phe	
185 190 195	

acc ttt gaa ttc agc cag tgg tca cag ctg gat gtt tgc gac atc cca	800
Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp Ile Pro	
200 205 210	

gag agc ttc cag aga agt gtt gat ggc gtc tct gaa tcc aag ttg caa	848
Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys Leu Gln	
215 220 225	

atc tgt gtt gaa cca act tcc caa aag ctg atg cca ggc agc aca ttg	896
Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser Thr Leu	
230 235 240	

gtt tta cag tgt gtt gct gtt gga agc cct att cct cac tac cag tgg	944
Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr Gln Trp	
245 250 255 260	

ttc aaa aat gaa tta cca tta aca cat gag acc aaa aag cta tac atg	992
Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu Tyr Met	
265 270 275	

gtg cct tat gtg gat ttg gaa cac caa gga acc tac tgg tgt cat gta	1040
Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys His Val	
280 285 290	

tat aat gat cga gac agt caa gat agc aag aag gta gaa atc atc ata	1088
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Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile Ile Ile
295 300 305

gga aga aca gat gag gca gtg gag tgc act gaa gat gaa tta aat aat 1136
Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu Asn Asn
310 315 320

ctt ggt cat cct gat aat aaa gag caa aca act gac cag cct ttg gcg 1184
Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro Leu Ala
325 330 335 340

aag gac aag gtt gcc ctt ttg ata gga aat atg aat tac cgg gag cac 1232
Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg Glu His
345 350 355

ccc aag ctc aaa gct cct ttg gtg gat gtg tac gaa ttg act aac tta 1280
Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr Asn Leu
360 365 370

ctg aga cag ctg gac ttc aaa gtg gtt tca ctg ttg gat ctt act gaa 1328
Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu Thr Glu
375 380 385

tat gag atg cgt aat gct gtg gat gag ttt tta ctc ctt tta gac aag 1376
Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu Asp Lys
390 395 400

gga gta tat ggg tta tta tat tat gca gga cat ggt tat gaa aat ttt 1424
Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu Asn Phe

405	410	415	420	
ggg aac agc ttc atg gtc ccc gtt gat gct cca aat cca tat agg tct				1472
Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr Arg Ser				
	425	430	435	
gaa aat tgt ctg tgt gta caa aat ata ctg aaa ttg atg caa gaa aaa				1520
Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln Glu Lys				
	440	445	450	
gaa act gga ctt aat gtg ttc tta ttg gat atg tgt agg aaa aga aat				1568
Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys Arg Asn				
	455	460	465	
gac tac gat gat acc att cca atc ttg gat gca cta aaa gtc acc gcc				1616
Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val Thr Ala				
	470	475	480	
aat att gtg ttt gga tat gcc acg tgt caa gga gca gaa gct ttt gaa				1664
Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala Phe Glu				
485	490	495	500	
atc cag cat tct gga ttg gca aat gga atc ttt atg aaa ttt tta aaa				1712
Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe Leu Lys				
	505	510	515	
gac aga tta tta gaa gat aag aaa atc act gtg tta ctg gat gaa gtt				1760
Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp Glu Val				
	520	525	530	

gca gaa gat atg ggt aag tgt cac ctt acc aaa ggc aaa cag gct cta 1808
 Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln Ala Leu

535

540

545

gag att cga agt agt tta tct gag aag aga gca ctt act gat cca ata 1856
 Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp Pro Ile

550

555

560

cag gga aca gaa tat tct gct gaa tct ctt gtg cgg aat cta cag tgg 1904
 Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu Gln Trp

565

570

575

580

gcc aag gct cat gaa ctt cca gaa agt atg tgt ctt aag ttt gac tgt 1952
 Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe Asp Cys

585

590

595

ggt gtt cag att caa tta gga ttt gca gct gag ttt tcc aat gtc atg 2000
 Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn Val Met

600

605

610

atc atc tat aca agt ata gtt tac aaa cca ccg gag ata ata atg tgt 2048
 Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile Met Cys

615

620

625

gat gcc tac gtt act gat ttt cca ctt gat cta gat att gat cca aaa 2096
 Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp Pro Lys

630

635

640

gat gca aat aaa ggc aca cct gaa gaa act ggc agc tac ttg gta tca 2144
 Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu Val Ser
 645 650 655 660

aag gat ctt ccc aag cat tgc ctc tat acc aga ctc agt tca ctg caa 2192
 Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser Leu Gln
 665 670 675

aaa tta aag gaa cat cta gtc ttc aca gta tgt tta tca tat cag tac 2240
 Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr Gln Tyr
 680 685 690

tca gga ttg gaa gat act gta gag gac aag cag gaa gtg aat gtt ggg 2288
 Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn Val Gly
 695 700 705

aaa cct ctc att gct aaa tta gac atg cat cga ggt ttg gga agg aag 2336
 Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly Arg Lys
 710 715 720

act tgc ttt caa act tgt ctt atg tct aat ggt cct tac cag agt tct 2384
 Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln Ser Ser
 725 730 735 740

gca gcc acc tca gga gga gca ggg cat tat cac tca ttg caa gac cca 2432
 Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln Asp Pro
 745 750 755

ttc cat ggt gtt tac cat tca cat cct ggt aat cca agt aat gtt aca 2480

Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn Val Thr
760 765 770

cca gca gat agc tgt cat tgc agc cgg act cca gat gca ttt att tca 2528
Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe Ile Ser
775 780 785

agt ttc gct cac cat gct tca tgt cat ttt agt aga agt aat gtg cca 2576
Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn Val Pro
790 795 800

gta gag aca act gat gaa ata cca ttt agt ttc tct gac agg ctc aga 2624
Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg Leu Arg
805 810 815 820

att tct gaa aaa tgacctcctt gtttttgaaa gttagcataa ttttagatgc 2676
Ile Ser Glu Lys

ctgtgaaata gtactgcact tacataaagt gagacattgt gaaaaggcaa atttgtatat 2736

gtagagaaag aatagtagta actgtttcat agcaaacttc aggactttga gatgttgaaa 2796

ttacattatt taattacaga cttcctcttt ct 2828

<210> 133

<211> 919

<212> PRT

<213> Homo sapiens

<400> 133

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Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro Val Ser

20 25 30

Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu Asn Lys

35 40 45

Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu Phe Asp

50 55 60

Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln Phe Lys

65 70 75 80

Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser Val Leu

85 90 95

Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile Leu Ile

100 105 110

Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys Ser Leu

115 120 125

Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val Arg Glu

130 135 140

Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly Asp Thr
145 150 155 160

Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg Leu Phe
165 170 175

Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly Glu Thr
180 185 190

Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr Asn Gly
195 200 205

Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu Val Arg
210 215 220

Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn Ser Glu
225 230 235 240

Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro Lys Thr
245 250 255

Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser Phe Tyr
260 265 270

Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu Leu Gly
275 280 285

Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala Val Ala
290 295 300

Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu Ala Leu
305 310 315 320

Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys Leu Pro
325 330 335

Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp Lys Thr
340 345 350

Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe Thr Ser
355 360 365

Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln Phe Gly
370 375 380

Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn Pro Ala
385 390 395 400

Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala Val Ile
405 410 415

Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu Ile Ala
420 425 430

Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr Ile Arg
435 440 445

Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala Val Lys
480/754

450	455	460
Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe Met Lys		
465	470	475 480
Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln Ser Lys		
	485	490 495
Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr Gln Gln		
	500	505 510
Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala Leu Ala		
	515	520 525
Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val Gly Ile		
	530	535 540
Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr Leu Ile		
545	550	555 560
Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln Glu Thr		
	565	570 575
Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr Ser Gln		
	580	585 590
Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln Leu Ser		
	595	600 605

Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro Arg His

610

615

620

Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val Val Ala

625

630

635

640

Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala Ala Asp

645

650

655

Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys Glu Ala

660

665

670

Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met Ser Ala

675

680

685

Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe Val Arg

690

695

700

Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser Leu Ala

705

710

715

720

Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile Leu Trp

725

730

735

Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly Val Glu

740

745

750

Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp Lys Asp

755

760

765

Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser Ser Ile
770 775 780

Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu Arg Asp
785 790 795 800

Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys Phe Val
805 810 815

Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr Lys Ser
820 825 830

Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr Ala Val
835 840 845

Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro Pro Leu
850 855 860

Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu Leu Phe
865 870 875 880

Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile Ile Lys
885 890 895

Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser Ser Thr
900 905 910

Ser Ser Ser Phe Leu Glu Val

<210> 134

<211> 3612

<212> DNA

<213> Homo sapiens

<220>

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<222> (427).. (3183)

<400> 134

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gagcaggctc ccgcctcgca ccgctgcccc gcgagcagct cctcttctcc cgaggcgcg 180

ggggcgcccc cgcgagcccc gcggctgaga cccgcagcc tggaggaggg ctgtccgggg 240

ctttggatgc tgctgctagg ggtggtggga gcagccgtgg gacgcgtggc cgggagcggg 300

ggtgacagcc tgggattccg ggggttctc ttccttgtec tctcctctc ctctctattc 360

ccagtgtggc cgtggctgac actaaagact ttgtagccat caaccgagt gcagtttcga 420

tgga aa atg aag gtt gca cgt ttt caa aaa ata cct aat ggt gaa aat 468

Met Lys Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu Asn

1	5	10	
gag aca atg att cct gta ttg aca tca aaa aaa gca agt gaa tta cca			516
Glu Thr Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro			
15	20	25	30
gtc agt gaa gtt gca agc att ctc caa gct gat ctt cag aat ggt cta			564
Val Ser Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu			
	35	40	45
aac aaa tgt gaa gtt agt cat agg cga gcc ttt cat ggc tgg aat gag			612
Asn Lys Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu			
	50	55	60
ttt gat att agt gaa gat gag cca ctg tgg aag aag tat att tct cag			660
Phe Asp Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln			
	65	70	75
ttt aaa aat ccc ctt att atg ctg ctt ctg gct tct gca gtc atc agt			708
Phe Lys Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser			
	80	85	90
gtt tta atg cat cag ttt gat gat gcc gtc agt atc act gtg gca ata			756
Val Leu Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile			
	95	100	105
ctt atc gtt gtt aca gtt gcc ttt gtt cag gaa tat cgt tca gaa aaa			804
Leu Ile Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys			
	115	120	125

tct ctt gaa gaa ttg agt aaa ctt gtg cca cca gaa tgc cat tgt gtg 852

Ser Leu Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val

130

135

140

cgt gaa gga aaa ttg gag cat aca ctt gcc cga gac ttg gtt cca ggt 900

Arg Glu Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly

145

150

155

gat aca gtt tgc ctt tct gtt ggg gat aga gtt cct gct gac tta cgc 948

Asp Thr Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg

160

165

170

ttg ttt gag gct gtg gat ctt tcc att gat gag tcc agc ttg aca ggt 996

Leu Phe Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly

175

180

185

190

gag aca acg cct tgt tct aag gtg aca gct cct cag cca gct gca act 1044

Glu Thr Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr

195

200

205

aat gga gat ctt gca tcg aga agt aac att gcc ttt atg gga aca ctg 1092

Asn Gly Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu

210

215

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gtc aga tgt ggc aaa gca aag ggt gtt gtc att gga aca gga gaa aat 1140

Val Arg Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn

225

230

235

tct gaa ttt ggg gag gtt ttt aaa atg atg caa gca gaa gag gca cca	1188
Ser Glu Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro	
240 245 250	

aaa acc cct ctg cag aag agc atg gac ctc tta gga aaa caa ctt tcc	1236
Lys Thr Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser	
255 260 265 270	

ttt tac tcc ttt ggt ata ata gga atc atc atg ttg gtt ggc tgg tta	1284
Phe Tyr Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu	
275 280 285	

ctg gga aaa gat atc ctg gaa atg ttt act att agt gta agt ttg gct	1332
Leu Gly Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala	
290 295 300	

gta gca gca att cct gaa ggt ctc ccc att gtg gtc aca gtg acg cta	1380
Val Ala Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu	
305 310 315	

gct ctt ggt gtt atg aga atg gtg aag aaa agg gcc att gtg aaa aag	1428
Ala Leu Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys	
320 325 330	

ctg cct att gtt gaa act ctg ggc tgc tgt aat gtg att tgt tca gat	1476
Leu Pro Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp	
335 340 345 350	

aaa act gga aca ctg acg aag aat gaa atg act gtt act cac ata ttt	1524
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Lys Thr Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe

355

360

365

act tca gat ggt ctg cat gct gag gtt act gga gtt ggc tat aat caa 1572

Thr Ser Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln

370

375

380

ttt ggg gaa gtg att gtt gat ggt gat gtt gtt cat gga ttc tat aac 1620

Phe Gly Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn

385

390

395

cca gct gtt agc aga att gtt gag gcg ggc tgt gtg tgc aat gat gct 1668

Pro Ala Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala

400

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410

gta att aga aac aat act cta atg ggg aag cca aca gaa ggg gcc tta 1716

Val Ile Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu

415

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425

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att gct ctt gca atg aag atg ggt ctt gat gga ctt caa caa gac tac 1764

Ile Ala Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr

435

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445

atc aga aaa gct gaa tac cct ttt agc tct gag caa aag tgg atg gct 1812

Ile Arg Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala

450

455

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gtt aag tgt gta cac cga aca cag cag gac aga cca gag att tgt ttt 1860

Val Lys Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe

465	470	475	
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Met Lys Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln			
480	485	490	
agc aaa ggg cag acc ttg aca ctt act cag cag cag aga gat gtg tac 1956			
Ser Lys Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr			
495	500	505	510
caa caa gag aag gca cgc atg ggc tca gcg gga ctc aga gtt ctt gct 2004			
Gln Gln Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala			
	515	520	525
ttg gct tct ggt cct gaa ctg gga cag ctg aca ttt ctt ggc ttg gtg 2052			
Leu Ala Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val			
	530	535	540
gga atc att gat cca cct aga act ggt gtg aaa gaa gct gtt aca aca 2100			
Gly Ile Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr			
	545	550	555
ctc att gcc tca gga gta tca ata aaa atg att act gga gat tca cag 2148			
Leu Ile Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln			
	560	565	570
gag act gca gtt gca atc gcc agt cgt ctg gga ttg tat tcc aaa act 2196			
Glu Thr Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr			
575	580	585	590

tcc cag tca gtc tca gga gaa gaa ata gat gca atg gat gtt cag cag 2244

Ser Gln Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln

595

600

605

ctt tca caa ata gta cca aag gtt gca gta ttt tac aga gct agc cca 2292

Leu Ser Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro

610

615

620

agg cac aag atg aaa att att aag tcg cta cag aag aac ggt tca gtt 2340

Arg His Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val

625

630

635

gta gcc atg aca gga gat gga gta aat gat gca gtt gct ctg aag gct 2388

Val Ala Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala

640

645

650

gca gac att gga gtt gcg atg ggc cag act ggt aca gat gtt tgc aaa 2436

Ala Asp Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys

655

660

665

670

gag gca gca gac atg atc cta gtg gat gat gat ttt caa acc ata atg 2484

Glu Ala Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met

675

680

685

tct gca atc gaa gag ggt aaa ggg att tat aat aac att aaa aat ttc 2532

Ser Ala Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe

690

695

700

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Val Arg Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser
705 710 715

ttg gct aca tta atg aac ttt cct aat cct ctc aat gcc atg cag att 2628
Leu Ala Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile
720 725 730

ttg tgg atc aat att att atg gat gga ccc cca gct cag agc ctt gga 2676
Leu Trp Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly
735 740 745 750

gta gaa cca gtg gat aaa gat gtc att cgt aaa cct cct cgc aac tgg 2724
Val Glu Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp
755 760 765

aaa gac agc att ttg act aaa aac ttg ata ctt aaa ata ctt gtt tca 2772
Lys Asp Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser
770 775 780

tca ata atc att gtt tgt ggg act ttg ttt gtc ttc tgg cgt gag cta 2820
Ser Ile Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu
785 790 795

cga gac aat gtg att aca cct cga gac aca aca atg acc ttc aca tgc 2868
Arg Asp Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys
800 805 810

ttt gtg ttt ttt gac atg ttc aat gca cta agt tcc aga tcc cag acc 2916

Phe Val Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr
815 820 825 830

aag tct gtg ttt gag att gga ctc tgc agt aat aga atg ttt tgc tat 2964
Lys Ser Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr
835 840 845

gca gtt ctt gga tcc atc atg gga caa tta cta gtt att tac ttt cct 3012
Ala Val Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro
850 855 860

ccg ctt cag aag gtt ttt cag act gag agc cta agc ata ctg gat ctg 3060
Pro Leu Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu
865 870 875

ttg ttt ctt ttg ggt ctc acc tca tca gtg tgc ata gtg gca gaa att 3108
Leu Phe Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile
880 885 890

ata aag aag gtt gaa agg agc agg gaa aag atc cag aag cat gtt agt 3156
Ile Lys Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser
895 900 905 910

tcg aca tca tca tct ttt ctt gaa gta tgatgcatat tgcattattt 3203
Ser Thr Ser Ser Ser Phe Leu Glu Val
915

tatttgcaaa ctaggaattg cagtctgagg atcatttaga agggcaagtt caagaggata 3263

tgaagatttg agaacttttt aactattcat tgactaaaaa tgaacattaa tgttaaagac 3323

ttaagacttt aacctgctgg cagtcccaaa tgaaattatg caactttgat atcatattcc 3383

ttgatttaaa ttggcttttg tgattgagtg aaactttata aagcatatgg tcagttattt 3443

aattaaaaag gcaaaacctg aaccaccttc tgcacttaaa gaagtctaac agtaciaata 3503

cactatctat cttagataga tatatTTTTT tttatTTTTa aatattgtac tatttatggt 3563

ggtggggctt tcttactaat acacaaataa atttaatcat ttcaaaggc 3612

<210> 135

<211> 382

<212> PRT

<213> Homo sapiens

<400> 135

Met Gly Ala Phe Leu Asp Lys Pro Lys Met Glu Lys His Asn Ala Gln

1 5 10 15

Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu Ser Ser Met Gln Gly Trp

20 25 30

Arg Val Glu Met Glu Asp Ala His Thr Ala Val Ile Gly Leu Pro Ser

35 40 45

Gly Leu Glu Ser Trp Ser Phe Phe Ala Val Tyr Asp Gly His Ala Gly

50		55		60
Ser Gln Val Ala Lys Tyr Cys Cys Glu His Leu Leu Asp His Ile Thr				
65		70		75
				80
Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly Ala Pro Ser Val Glu Asn				
	85		90	
				95
Val Lys Asn Gly Ile Arg Thr Gly Phe Leu Glu Ile Asp Glu His Met				
	100		105	
				110
Arg Val Met Ser Glu Lys Lys His Gly Ala Asp Arg Ser Gly Ser Thr				
	115		120	
				125
Ala Val Gly Val Leu Ile Ser Pro Gln His Thr Tyr Phe Ile Asn Cys				
	130		135	
				140
Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn Arg Lys Val His Phe Phe				
145		150		155
				160
Thr Gln Asp His Lys Pro Ser Asn Pro Leu Glu Lys Glu Arg Ile Gln				
	165		170	
				175
Asn Ala Gly Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala				
	180		185	
				190
Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr Lys Cys Val His Gly Lys				
	195		200	
				205

Gly Pro Thr Glu Gln Leu Val Ser Pro Glu Pro Glu Val His Asp Ile
210 215 220

Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile Ile Leu Ala Cys Asp Gly
225 230 235 240

Ile Trp Asp Val Met Gly Asn Glu Glu Leu Cys Asp Phe Val Arg Ser
245 250 255

Arg Leu Glu Val Thr Asp Asp Leu Glu Lys Val Cys Asn Glu Val Val
260 265 270

Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp Asn Met Ser Val Ile Leu
275 280 285

Ile Cys Phe Pro Asn Ala Pro Lys Val Ser Pro Glu Ala Val Lys Lys
290 295 300

Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys Arg Val Glu Glu Ile Ile
305 310 315 320

Lys Lys Gln Gly Glu Gly Val Pro Asp Leu Val His Val Met Arg Thr
325 330 335

Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro Pro Gly Gly Glu Leu Ala
340 345 350

Ser Lys Arg Asn Val Ile Glu Ala Val Tyr Asn Arg Leu Asn Pro Tyr
355 360 365

Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr Asp Asp Met Trp

370

375

380

<210> 136

<211> 2467

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (444)..(1589)

<400> 136

acgggagcgc gcgcgggagc tagagagcag tgggtctcggc gctcgtccgg cccgcagctt 60

cgggtcctca ggcggtctgtt gctccggaac ggggtggttg ggaggggggg gtgggggggac 120

tctagacagc tgaggcgcga aagcgatgag tcctcggtc ttcctcctcc ttctccggga 180

cccgtctctt gcctccctct ccaacgcccg gatgatctga gccgcgaggg cgccgacagc 240

cggggggccc gacgcagccc ggctcctccc ctctccgcc ctttccccag cctgacctgg 300

cccgcgctg cagcggtgac ccctcccccg gctgccgccg tcgccgccgc ggtgaccccc 360

tccccggctg ccgccgccgc cgcctcggcc gaccagggac ctgcccgcct gcggtctgctc 420

cggacctaga ggatcaagac ata atg gga gca ttt tta gac aag cca aag atg 473

Met Gly Ala Phe Leu Asp Lys Pro Lys Met

1

5

10

gaa aag cat aat gcc cag ggg cag ggt aat ggg ttg cga tat ggg cta 521

Glu Lys His Asn Ala Gln Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu

15

20

25

agc agc atg caa ggc tgg cgt gtt gaa atg gag gat gca cat acg gct 569

Ser Ser Met Gln Gly Trp Arg Val Glu Met Glu Asp Ala His Thr Ala

30

35

40

gtg atc ggt ttg cca agt gga ctt gaa tcg tgg tca ttc ttt gct gtg 617

Val Ile Gly Leu Pro Ser Gly Leu Glu Ser Trp Ser Phe Phe Ala Val

45

50

55

tat gat ggg cat gct ggt tct cag gtt gcc aaa tac tgc tgt gag cat 665

Tyr Asp Gly His Ala Gly Ser Gln Val Ala Lys Tyr Cys Cys Glu His

60

65

70

ttg tta gat cac atc acc aat aac cag gat ttt aaa ggg tct gca gga 713

Leu Leu Asp His Ile Thr Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly

75

80

85

90

gca cct tct gtg gaa aat gta aag aat gga atc aga aca ggt ttt ctg 761

Ala Pro Ser Val Glu Asn Val Lys Asn Gly Ile Arg Thr Gly Phe Leu

95

100

105

gag att gat gaa cac atg aga gtt atg tca gag aag aaa cat ggt gca 809

Glu Ile Asp Glu His Met Arg Val Met Ser Glu Lys Lys His Gly Ala

110

115

120

gat aga agt ggg tca aca gct gta ggt gtc tta att tct ccc caa cat 857

Asp Arg Ser Gly Ser Thr Ala Val Gly Val Leu Ile Ser Pro Gln His

125

130

135

act tat ttc att aac tgt gga gac tca aga ggt tta ctt tgt agg aac 905

Thr Tyr Phe Ile Asn Cys Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn

140

145

150

agg aaa gtt cat ttc ttc aca caa gat cac aaa cca agt aat ccg ctg 953

Arg Lys Val His Phe Phe Thr Gln Asp His Lys Pro Ser Asn Pro Leu

155

160

165

170

gag aaa gaa cga att cag aat gca ggt ggc tct gta atg att cag cgt 1001

Glu Lys Glu Arg Ile Gln Asn Ala Gly Gly Ser Val Met Ile Gln Arg

175

180

185

gtg aat ggc tct ctg gct gta tcg agg gcc ctt ggg gat ttt gat tac 1049

Val Asn Gly Ser Leu Ala Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr

190

195

200

aaa tgt gtc cat gga aaa ggt cct act gag cag ctt gtc tca cca gag 1097

Lys Cys Val His Gly Lys Gly Pro Thr Glu Gln Leu Val Ser Pro Glu

205

210

215

cct gaa gtc cat gat att gaa aga tct gaa gaa gat gat cag ttc att 1145

Pro Glu Val His Asp Ile Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile

220	225	230	
atc ctt gca tgt gat ggt atc tgg gat gtt atg gga aat gaa gag ctc			1193
Ile Leu Ala Cys Asp Gly Ile Trp Asp Val Met Gly Asn Glu Glu Leu			
235	240	245	250
tgt gat ttt gta aga tcc aga ctt gaa gtc act gat gac ctt gag aaa			1241
Cys Asp Phe Val Arg Ser Arg Leu Glu Val Thr Asp Asp Leu Glu Lys			
	255	260	265
gtt tgc aat gaa gta gtc gac acc tgt ttg tat aag gga agt cga gac			1289
Val Cys Asn Glu Val Val Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp			
	270	275	280
aac atg agt gtg att ttg atc tgt ttt cca aat gca ccc aaa gta tcg			1337
Asn Met Ser Val Ile Leu Ile Cys Phe Pro Asn Ala Pro Lys Val Ser			
	285	290	295
cca gaa gca gtg aag aag gag gca gag ttg gac aag tac ctg gaa tgc			1385
Pro Glu Ala Val Lys Lys Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys			
	300	305	310
aga gta gaa gaa atc ata aag aag cag ggg gaa ggc gtc ccc gac tta			1433
Arg Val Glu Glu Ile Ile Lys Lys Gln Gly Glu Gly Val Pro Asp Leu			
	315	320	325
			330
gtc cat gtg atg cgc aca tta gcg agt gag aac atc ccc agc ctc cca			1481
Val His Val Met Arg Thr Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro			
	335	340	345

cca ggg ggt gaa ttg gca agc aag agg aat gtt att gaa gcc gtt tac 1529
Pro Gly Gly Glu Leu Ala Ser Lys Arg Asn Val Ile Glu Ala Val Tyr

350

355

360

aat aga ctg aat cct tac aaa aat gac gac act gac tct aca tca aca 1577
Asn Arg Leu Asn Pro Tyr Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr

365

370

375

gat gat atg tgg taaaactgct catctagcca tggagtttac cttcacctcc 1629
Asp Asp Met Trp

380

aaaggagagt acagctcaac tttgttgaaa cttttaacat ccatacctcaa ctttaaggaa 1689

ggggatatga catgggtgag aatgattaca tcagagaact tcagcagtac aacagctagc 1749

ccagaactga tttttttttt ttttttgtaa atttgagact tatgtaagcg tgatttcaaa 1809

ccataattcg tgttgtaa at cagactccag caatttttgt tgtatgattt tgtttttttg 1869

taaagtgtaa ttgtccttgt acaaaatgct catattta at tatgaactgc tttaa atcac 1929

tatcaaagtt acaagaa atg tttggccttat tgtgtgatgc aacagatata tagccctttc 1989

aagtcatgtt gtgtttggac ttgggggttg aacagggaga gcagcagcca tgtcagctac 2049

acgctcaa at gtgcagatga ttatggaaaa taacctcaaa atcttacaaa gctgaacatc 2109

caaggagtta ttgaaaacta tcttaaattgt tcttggtagg ggagttggca ttgttgataa 2169

agccagtccc ttcatttaac tgtctttcag gatgttcctt cgttgtttcc atgagtattg 2229

caggtaataa tacagtgtat tcataagaat ctcaatcttg gggctaaatg ccttgtttct 2289

ttgcacctct tttcaagtcc ttacatttaa ttactaattg ataagcagca gcttcctaca 2349

tatagtagga aactgccaca tttttgctat catgattggc tgggcctgct gctgttccta 2409

gtaagatatt ctgaattcca ttttatcaat aaagcttgat ttaacaaaca agaaactt 2467

<210> 137

<211> 358

<212> PRT

<213> Homo sapiens

<400> 137

Met Met Gln Arg Val Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val

1 5 10 15

Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp

20 25 30

Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu

35 40 45

Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val

50	55	60
Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg		
65	70	75 80
Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn		
85	90	95
Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser		
100	105	110
Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser		
115	120	125
Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met		
130	135	140
Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala		
145	150	155 160
Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser		
165	170	175
Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr		
180	185	190
Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln		
195	200	205

Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln
210 215 220

Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro
225 230 235 240

Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln
245 250 255

Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln
260 265 270

Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr
275 280 285

Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln
290 295 300

Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly
305 310 315 320

Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro
325 330 335

Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln
340 345 350

Pro Gly Pro Gly Tyr Arg
355

<210> 138

<211> 1519

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (11)..(1084)

<400> 138

attagtgcta atg atg caa cga gtt ttc aga gga aaa ctt ctg agt aat 49

Met Met Gln Arg Val Phe Arg Gly Lys Leu Leu Ser Asn

1

5

10

gat gaa gta aca ata aag tat aaa gat gaa gat gga gat ctt ata aca 97

Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr

15

20

25

att ttt gat agt tct gac ctt tcc ttt gca att cag tgc agt agg ata 145

Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile

30

35

40

45

ctg aaa ctg aca tta ttt gtt aat ggc cag cca aga ccc ctt gaa tca 193

Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser

50

55

60

agt cag gtg aaa tat ctc cgt cga gaa ctg ata gaa ctt cga aat aaa 241

Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys

65

70

75

gtg aat cgt tta ttg gat agc ttg gaa cca cct gga gaa cca gga cct 289

Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro

80

85

90

tcc acc aat att cct gaa aat gat act gtg gat ggt agg gaa gaa aag 337

Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys

95

100

105

tct gct tct gat tct tct gga aaa cag tct act cag gtt atg gca gca 385

Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala

110

115

120

125

agt atg tct gct ttt gat cct tta aaa aac caa gat gaa atc aat aaa 433

Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys

130

135

140

aat gtt atg tca gcg ttt ggc tta aca gat gat cag gtt tca ggg cca 481

Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro

145

150

155

ccc agt gct cct gca gaa gat cgt tca gga aca ccc gac agc att gct 529

Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala

160

165

170

tcc tcc tcc tca gca gct cac cca cca ggc gtt cag cca cag cag cca 577

Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro

175	180	185	
cca tat aca gga gct cag act caa gca ggt cag atg tac caa cag tac	625		
Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr			
190	195	200	205
cag caa cag gcc ggc tat ggt gca cag cag ccg cag gct cca cct cag	673		
Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln			
210	215	220	
cag cct caa cag tat ggt att cag tat tca gca agc tat agt cag cag	721		
Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln			
225	230	235	
act gga ccc caa caa cct cag cag ttc cag gga tat ggc cag caa cca	769		
Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro			
240	245	250	
act tcc cag gca cca gct cct gcc ttt tct ggt cag cct caa caa ctg	817		
Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu			
255	260	265	
cct gct cag ccg cca cag cag tac cag gcg agc aat tat cct gca caa	865		
Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln			
270	275	280	285
act tac act gcc caa act tct cag cct act aat tat act gtg gct cct	913		
Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro			
290	295	300	

gcc tct caa cct gga atg gct cca agc caa cct ggg gcc tat caa cca 961

Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro

305

310

315

aga cca ggt ttt act tca ctt cct gga agt acc atg acc cct cct cca 1009

Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro

320

325

330

agt ggg cct aat cct tat gcg cgt aac cgt cct ccc ttt ggt cag ggc 1057

Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly

335

340

345

tat acc caa cct gga cct ggt tat cga taaggaggct cctctacacc 1104

Tyr Thr Gln Pro Gly Pro Gly Tyr Arg

350

355

aattaatgta gctgctagct attggcctcc caaaagactc cagtactatt ttaatttgta 1164

ttgaagaagt tcagaaattht aaaagcagag cattttttat gatattcattg ttggtgttaa 1224

ttgaaagtat aatttgctgg aacacaaaga ccaaaatgaa agttttttcc tccctgctta 1284

aaaatgtagc agcttcttag ttactttgga acactactct tacatgtata aagtgattga 1344

cttgactttc tagcttcct tgtccggagg atattaaaat gctagggtga ggtttagcca 1404

tcttacttgg ctttttacta ttaacatgat gtactaaagt agagcccttt gagaatacaa 1464

gatattatgt ataaaatgta acactgatga taggttaata aagatgattg aatcc 1519

<210> 139

<211> 396

<212> PRT

<213> Homo sapiens

<400> 139

Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu Ile Val Lys Ala Gln

1 5 10 15

Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His Asn Glu Asp Ile Thr

20 25 30

Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val Phe Arg Gly Lys Leu

35 40 45

Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp

50 55 60

Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys

65 70 75 80

Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro

85 90 95

Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu

100 105 110

508/754

Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu
115 120 125

Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg
130 135 140

Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val
145 150 155 160

Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu
165 170 175

Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val
180 185 190

Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp
195 200 205

Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro
210 215 220

Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr
225 230 235 240

Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala
245 250 255

Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr

260	265	270
Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly		
275	280	285
Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro		
290	295	300
Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr		
305	310	315
		320
Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr		
325	330	335
Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala		
340	345	350
Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr		
355	360	365
Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe		
370	375	380
Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr Arg		
385	390	395

<210> 140

<211> 1641

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (19)..(1206)

<400> 140

aacatcctgg agtccacc atg aac gga cag ttg gat cta agt ggg aag cta 51

Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu

1 5 10

atc gtc aaa gct caa ctt ggg gag gat att cgg cga att cct att cat 99

Ile Val Lys Ala Gln Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His

15 20 25

aat gaa gat att act tat gat gaa tta gtg cta atg atg caa cga gtt 147

Asn Glu Asp Ile Thr Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val

30 35 40

ttc aga gga aaa ctt ctg agt aat gat gaa gta aca ata aag tat aaa 195

Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys

45 50 55

gat gaa gat gga gat ctt ata aca att ttt gat agt tct gac ctt tcc 243

Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser

60 65 70 75

ttt gca att cag tgc agt agg ata ctg aaa ctg aca tta ttt gtt aat 291

Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn

80

85

90

ggc cag cca aga ccc ctt gaa tca agt cag gtg aaa tat ctc cgt cga 339

Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg

95

100

105

gaa ctg ata gaa ctt cga aat aaa gtg aat cgt tta ttg gat agc ttg 387

Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu

110

115

120

gaa cca cct gga gaa cca gga cct tcc acc aat att cct gaa aat gat 435

Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp

125

130

135

act gtg gat ggt agg gaa gaa aag tct gct tct gat tct tct gga aaa 483

Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys

140

145

150

155

cag tct act cag gtt atg gca gca agt atg tct gct ttt gat cct tta 531

Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu

160

165

170

aaa aac caa gat gaa atc aat aaa aat gtt atg tca gcg ttt ggc tta 579

Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu

175

180

185

aca gat gat cag gtt tca ggg cca ccc agt gct cct gca gaa gat cgt 627

Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg

190	195	200	
tca gga aca ccc gac agc att gct tcc tcc tcc tca gca gct cac cca	675		
Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro			
205	210	215	
cca ggc gtt cag cca cag cag cca cca tat aca gga gct cag act caa	723		
Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln			
220	225	230	235
gca ggt cag atg tac caa cag tac cag caa cag gcc ggc tat ggt gca	771		
Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala			
240	245	250	
cag cag ccg cag gct cca cct cag cag cct caa cag tat ggt att cag	819		
Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln			
255	260	265	
tat tca gca agc tat agt cag cag act gga ccc caa caa cct cag cag	867		
Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln			
270	275	280	
ttc cag gga tat ggc cag caa cca act tcc cag gca cca gct cct gcc	915		
Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala			
285	290	295	
ttt tct ggt cag cct caa caa ctg cct gct cag ccg cca cag cag tac	963		
Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr			
300	305	310	315

cag gcg agc aat tat cct gca caa act tac act gcc caa act tct cag 1011

Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln

320

325

330

cct act aat tat act gtg gct cct gcc tct caa cct gga atg gct cca 1059

Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro

335

340

345

agc caa cct ggg gcc tat caa cca aga cca ggt ttt act tca ctt cct 1107

Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro

350

355

360

gga agt acc atg acc cct cct cca agt ggg cct aat cct tat gcg cgt 1155

Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg

365

370

375

aac cgt cct ccc ttt ggt cag ggc tat acc caa cct gga cct ggt tat 1203

Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr

380

385

390

395

cga taaggaggct cctctacacc aattaatgta gctgctagct attggcctcc 1256

Arg

caaaagactc cagtactatt ttaatttgta ttgaagaagt tcagaaattt aaaagcagag 1316

cattttttat gatattcattg ttggtgttaa ttgaaagtat aatttgctgg aacacaaaga 1376

ccaaaatgaa agttttttcc tcctgctta aaaatgtagc agcttcttag ttactttgga 1436

acactactct tacatgtata aagtgattga cttgactttc tagcttccct tgtccggagg 1496

atattaaaat gctaggggtga ggtttagcca tcttacttgg ctttttacta ttaacatgat 1556

gtactaaagt agagcccttt gagaatacaa gatattatgt ataaaatgta acactgatga 1616

taggttaata aagatgattg aatcc 1641

<210> 141

<211> 323

<212> PRT

<213> Homo sapiens

<400> 141

Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro Ala Val Pro

1 5 10 15

Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu Gln Ile Thr

20 25 30

Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn

35 40 45

Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro

50 55 60

Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly

515/754

65		70		75		80									
Ser	Trp	Gly	Pro	Glu	Glu	Arg	Lys	Thr	His	Met	Pro	Phe	Gln	Lys	Gly
				85					90					95	
Met	Pro	Phe	Asp	Leu	Cys	Phe	Leu	Val	Gln	Ser	Ser	Asp	Phe	Lys	Val
				100					105					110	
Met	Val	Asn	Gly	Ile	Leu	Phe	Val	Gln	Tyr	Phe	His	Arg	Val	Pro	Phe
				115					120					125	
His	Arg	Val	Asp	Thr	Ile	Ser	Val	Asn	Gly	Ser	Val	Gln	Leu	Ser	Tyr
				130					135					140	
Ile	Ser	Phe	Gln	Pro	Pro	Gly	Val	Trp	Pro	Ala	Asn	Pro	Ala	Pro	Ile
				145					150					155	
Thr	Gln	Thr	Val	Ile	His	Thr	Val	Gln	Ser	Ala	Pro	Gly	Gln	Met	Phe
				165					170					175	
Ser	Thr	Pro	Ala	Ile	Pro	Pro	Met	Met	Tyr	Pro	His	Pro	Ala	Tyr	Pro
				180					185					190	
Met	Pro	Phe	Ile	Thr	Thr	Ile	Leu	Gly	Gly	Leu	Tyr	Pro	Ser	Lys	Ser
				195					200					205	
Ile	Leu	Leu	Ser	Gly	Thr	Val	Leu	Pro	Ser	Ala	Gln	Arg	Phe	His	Ile
				210					215					220	

Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe
225 230 235 240

Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly
245 250 255

Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln
260 265 270

Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala
275 280 285

Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu
290 295 300

Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His
305 310 315 320

Val Gln Thr

<210> 142

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (72)..(1040)

<400> 142

aagtcgttcc ctctacaaag gacttcctag tgggtgtgaa aggcagcggg gccacagag 60

gcggcggaga g atg gcc ttc agc ggt tcc cag gct ccc tac ctg agt cca 110

Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro

1

5

10

gct gtc ccc ttt tct ggg act att caa gga ggt ctc cag gac gga ctt 158

Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu

15

20

25

cag atc act gtc aat ggg acc gtt ctc agc tcc agt gga acc agg ttt 206

Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe

30

35

40

45

gct gtg aac ttt cag act ggc ttc agt gga aat gac att gcc ttc cac 254

Ala Val Asn Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His

50

55

60

ttc aac cct cgg ttt gaa gat gga ggg tac gtg gtg tgc aac acg agg 302

Phe Asn Pro Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg

65

70

75

cag aac gga agc tgg ggg ccc gag gag agg aag aca cac atg cct ttc 350

Gln Asn Gly Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe

80

85

90

cag aag ggg atg ccc ttt gac ctc tgc ttc ctg gtg cag agc tca gat 398
 Gln Lys Gly Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp
 95 100 105

ttc aag gtg atg gtg aac ggg atc ctc ttc gtg cag tac ttc cac cgc 446
 Phe Lys Val Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg
 110 115 120 125

gtg ccc ttc cac cgt gtg gac acc atc tcc gtc aat ggc tct gtg cag 494
 Val Pro Phe His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln
 130 135 140

ctg tcc tac atc agc ttc cag cct ccc ggc gtg tgg cct gcc aac ccg 542
 Leu Ser Tyr Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro
 145 150 155

gct ccc att acc cag aca gtc atc cac aca gtg cag agc gcc cct gga 590
 Ala Pro Ile Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly
 160 165 170

cag atg ttc tct act ccc gcc atc cca cct atg atg tac ccc cac ccc 638
 Gln Met Phe Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro
 175 180 185

gcc tat ccg atg cct ttc atc acc acc att ctg gga ggg ctg tac cca 686
 Ala Tyr Pro Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro
 190 195 200 205

tcc aag tcc atc ctc ctg tca ggc act gtc ctg ccc agt gct cag agg 734

Ser Lys Ser Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg	
210	215 220
ttc cac atc aac ctg tgc tct ggg aac cac atc gcc ttc cac ctg aac	782
Phe His Ile Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn	
225	230 235
ccc cgt ttt gat gag aat gct gtg gtc cgc aac acc cag atc gac aac	830
Pro Arg Phe Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn	
240	245 250
tcc tgg ggg tct gag gag cga agt ctg ccc cga aaa atg ccc ttc gtc	878
Ser Trp Gly Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val	
255	260 265
cgt ggc cag agc ttc tca gtg tgg atc ttg tgt gaa gct cac tgc ctc	926
Arg Gly Gln Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu	
270	275 280 285
aag gtg gcc gtg gat ggt cag cac ctg ttt gaa tac tac cat cgc ctg	974
Lys Val Ala Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu	
290	295 300
agg aac ctg ccc acc atc aac aga ctg gaa gtg ggg ggc gac atc cag	1022
Arg Asn Leu Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln	
305	310 315
ctg acc cat gtg cag aca taggcggcctt cctggccctg gggccggggg	1070
Leu Thr His Val Gln Thr	

ctggggtgtg gggcagtctg ggtcctctca tcatcccccac ttcccaggcc cagcctttcc 1130

aaccctgcct gggatctggg cttaaatgca gaggccatgt ccttgtctgg tcctgtttct 1190

ggctacagcc accctggaac ggagaaggca gctgacgggg attgccttcc tcagccgcag 1250

cagcacctgg ggctccagct gctggaatcc taccatccca ggaggcaggc acagccaggg 1310

agaggggagg agtgggcagt gaagatgaag ccccatgctc agtcccctcc catcccccac 1370

gcagctccac ccagtccca agccaccagc tgtctgctcc tgggtgggagg tggcctcctc 1430

agcccctcct ctctgacctt taacctcact ctcaccttgc accgtgcacc aacccttcac 1490

ccctcctgga aagcaggcct gatggcttcc cactggcctc caccacctga ccagagtgtt 1550

ctcttcagag gactggctcc tttcccagtg tccttaaaat aaagaaatga aaatgcttgt 1610

tggcac 1616

<210> 143

<211> 136

<212> PRT

<213> Homo sapiens

<400> 143

Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile
1 5 10 15

Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly
20 25 30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
35 40 45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
50 55 60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
65 70 75 80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
85 90 95

Pro Leu Pro His Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His
100 105 110

Gly His Leu Ser Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe
115 120 125

Leu Gln Pro Leu Met His Cys Val
130 135

<210> 144

<211> 1252

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225)..(632)

<400> 144

acaatcacag ctccgggcat tgggggaacc cgagccggct gcgccggggg aatccgtgcg 60

ggcgcccttc gtcccgggtcc catcctcgcc gcgctccagc acctctgaag ttttcagcgc 120

cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcacct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284

Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

5

10

15

20

ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct 332

Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala

25

30

35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380

Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp

40	45	50	
gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc			428
Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro			
55	60	65	
aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa			476
Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu			
70	75	80	
att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac			524
Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His			
85	90	95	100
atg gct ctt agc tgt ggt ttc ttg gac cag cgg cat gga cat ttg tca			572
Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His Gly His Leu Ser			
105	110	115	
gtt tgc ctt ctg acg gta gct ttt gga gga aga ttc ctg cag cca cta			620
Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe Leu Gln Pro Leu			
120	125	130	
atg cat tgt gta tgataacaaa aactctggta tgacacattt tctgtgatca			672
Met His Cys Val			
135			
ttgttaatta gtgacatagt aacatctgta gcagctgggt agtaaacctc atgtgggggt			732
ggggtggggg tgtattcctt gggggatggt ttgggccgaa tggggagtgg aatatttgac			792

atttttcctg ttttaaattc taggatatagat ttttaacatcc tttgcggtcc cagtccaagg 852
 taggctgggtg tcatagtctt ctcactccta atccatgacc actgtttttt tcctatttat 912
 atcaccaggt agcctactga gttaatatatt aagttgtcaa tagataagtg tccctgtttt 972
 gtggcataat ataactgaat ttcatgagaa gatttattcc accaggggta tttcagcttt 1032
 gaaaccaaatt ctgtgtatct aataactaacc aatctgttgg atgtgggttt taaaaaatgt 1092
 ttgctaaact acccaagtaa gatttactgt attaaatggc cttcgggtct gaaaagcttt 1152
 tttaacctct tgcttaaaat gcgtttttatt ttgataagat acttcaaata gcctccaaaa 1212
 gtgtagatcc aatcacttaa ataaacctgt atgtatatgc 1252

<210> 145

<211> 468

<212> PRT

<213> Homo sapiens

<400> 145

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp

1

5

10

15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Phe

20

25

30

Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln
35 40 45

Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg
50 55 60

Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro
65 70 75 80

Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu
85 90 95

Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser
100 105 110

Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu
115 120 125

Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu
130 135 140

Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met
145 150 155 160

Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp
165 170 175

Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val

	180	185	190
Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu			
195	200	205	
Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp			
210	215	220	
Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile			
225	230	235	240
Phe Cys Gly Glu His Met Met Asp Gln His Glu Arg Asn His Ile Ala			
245	250	255	
Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu			
260	265	270	
Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe			
275	280	285	
Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe			
290	295	300	
Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys			
305	310	315	320
Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser			
325	330	335	

Leu Pro Ala Met Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile
340 345 350

Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met
355 360 365

Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys
370 375 380

Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile
385 390 395 400

Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala
405 410 415

Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu
420 425 430

Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr
435 440 445

Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala
450 455 460

Ala Ser Gly Ile
465

<210> 146

<211> 1943

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (379).. (1782)

<400> 146

acaatcacag ctccgggcat tgggggaacc cgagccggct gcgccggggg aatccgtgcg 60

ggcgccttcc gtcccgggtcc catcctcgcc gcgtccagc acctctgaag ttttgcagcg 120

cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaaatggct ggggcaatta 240

tagaaaacat gagcaccaag aagctgtgca ttgttggtgg gattctgctc gtgttccaaa 300

tcatgcctt tctggtggga ggcttgattg ctccagggcc cacaacggca gtgtcctaca 360

tgtcggtgaa atgtgtgg atg ccc gta aga acc atc aca aga caa aat ggt 411

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly

1

5

10

tcg tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag 459

Ser Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys

15

20

25

agg caa ttc caa ttc atg ctg ttt atc ctg cag ctg gac att gcc ttc 507
 Arg Gln Phe Gln Phe Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe

30 35 40

aag cta aac aac caa atc aga gaa aat gca gaa gtc tcc atg gac gtt 555
 Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val

45 50 55

tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg act gaa atg gcc 603
 Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala

60 65 70 75

cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc aca tct ccc aag 651
 His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys

80 85 90

act cca gag cat gag ggc cgt tac tat gaa tgt gat gtc ctt cct ttc 699
 Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe

95 100 105

atg gaa att ggg tct gtg gcc cat aag ttt tac ctt tta aac atc cgg 747
 Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg

110 115 120

ctg cct gtg aat gag aag aag aaa atc aat gtg gga att ggg gag ata 795
 Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile

125 130 135

aag gat atc cgg ttg gtg ggg atc cac caa aat gga ggc ttc acc aag 843

Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys
140 145 150 155

gtg tgg ttt gcc atg aag acc ttc ctt acg ccc agc atc ttc atc att 891
Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile
160 165 170

atg gtg tgg tat tgg agg agg atc acc atg atg tcc cga ccc cca gtg 939
Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val
175 180 185

ctt ctg gaa aaa gtc atc ttt gcc ctt ggg att tcc atg acc ttt atc 987
Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile
190 195 200

aat atc cca gtg gaa tgg ttt tcc atc ggg ttt gac tgg acc tgg atg 1035
Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met
205 210 215

ctg ctg ttt ggt gac atc cga cag ggc atc ttc tat gcg atg ctt ctg 1083
Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu
220 225 230 235

tcc ttc tgg atc atc ttc tgt ggc gag cac atg atg gat cag cac gag 1131
Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp Gln His Glu
240 245 250

cgg aac cac atc gca ggg tat tgg aag caa gtc gga ccc att gcc gtt 1179
Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val

255	260	265	
ggc tcc ttc tgc ctc ttc ata ttt gac atg tgt gag aga ggg gta caa			1227
Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln			
270	275	280	
ctc acg aat ccc ttc tac agt atc tgg act aca gac att gga aca gag			1275
Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu			
285	290	295	
ctg gcc atg gcc ttc atc atc gtg gct gga atc tgc ctc tgc ctc tac			1323
Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr			
300	305	310	315
ttc ctg ttt cta tgc ttc atg gta ttt cag gtg ttt cgg aac atc agt			1371
Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser			
320	325	330	
ggg aag cag tcc agc ctg cca gct atg agc aaa gtc cgg cgg cta cac			1419
Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg Arg Leu His			
335	340	345	
tat gag ggg cta att ttt agg ttc aag ttc ctc atg ctt atc acc ttg			1467
Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu			
350	355	360	
gcc tgc gct gcc atg act gtc atc ttc ttc atc gtt agt cag gta acg			1515
Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr			
365	370	375	

gaa ggc cat tgg aaa tgg ggc ggc gtc aca gtc caa gtg aac agt gcc 1563
 Glu Gly His Trp Lys Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala
 380 385 390 395

ttt ttc aca ggc atc tat ggg atg tgg aat ctg tat gtc ttt gct ctg 1611
 Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu
 400 405 410

atg ttc ttg tat gca cca tcc cat aaa aac tat gga gaa gac cag tcc 1659
 Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser
 415 420 425

aat gga atg caa ctc cca tgt aaa tcg agg gaa gat tgt gct ttg ttt 1707
 Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe
 430 435 440

gtt tcg gaa ctt tat caa gaa ttg ttc agc gct tcg aaa tat tcc ttc 1755
 Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe
 445 450 455

atc aat gac aac gca gct tct ggt att tgagtcaaca aggcaacaca 1802
 Ile Asn Asp Asn Ala Ala Ser Gly Ile
 460 465

tgtttatcag ctttgcatTT gcagttgtca cagtcacatt gattgtactt gtatacgcac 1862

acaaatacac tcatttagcc tttatctcaa aatgttaaT ataaggaaaa aagcgtcaac 1922

aataaatatt ctttgagtat t

1943

<210> 147

<211> 460

<212> PRT

<213> Homo sapiens

<400> 147

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp

1 5 10 15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Gly

20 25 30

Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr Phe Pro Ser Pro

35 40 45

Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr

50 55 60

Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr

65 70 75 80

Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val

85 90 95

Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu

100 105 110

534/754

Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile
115 120 125

Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly
130 135 140

Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile
145 150 155 160

Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg
165 170 175

Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met
180 185 190

Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp
195 200 205

Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala
210 215 220

Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp
225 230 235 240

Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro
245 250 255

Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg

260	265	270
Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile		
275	280	285
Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu		
290	295	300
Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg		
305	310	315 320
Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg		
325	330	335
Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu		
340	345	350
Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser		
355	360	365
Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile Thr Val Gln Val		
370	375	380
Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val		
385	390	395 400
Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu		
405	410	415

Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys

420

425

430

Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys

435

440

445

Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile

450

455

460

<210> 148

<211> 1919

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (376).. (1755)

<400> 148

atcacagctc cgggcattgg gggaacccega gccggctgcg ccgggggaat ccgtgcgggc 60

gccttcgctc ccggtcccat cctcgccgcg ctccagcacc tctgaagttt tgcagcgccc 120

agaaaggagg cgaggaagga gggagtgtat gagaggaggg agcaaaaagc tcaccctaaa 180

acatttattt caaggagaaa agaaaaaggg ggggcgcaaa aatggctggg gcaattatag 240

aaaacatgag caccaagaag ctgtgcattg ttggtgggat tctgctcgtg ttccaaatca 300

tcgcctttct ggtgggaggc ttgattgctc cagggccccac aacggcagtg tcctacatgt 360

cggtgaaatg tgtgg atg ccc gta aga acc atc aca aga caa aat ggt tcg 411

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser

1

5

10

tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag agg 459

Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg

15

20

25

caa ttc caa ggg aaa ttg aag cca atg aca tcg tgt ttt ctg ttc aca 507

Gln Phe Gln Gly Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr

30

35

40

ttc ccc tcc ccc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt 555

Phe Pro Ser Pro Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe

45

50

55

60

gct gag tgg act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa 603

Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys

65

70

75

tgc acc ttc aca tct ccc aag act cca gag cat gag ggc cgt tac tat 651

Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr

80

85

90

gaa tgt gat gtc ctt cct ttc atg gaa att ggg tct gtg gcc cat aag 699

Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys

95	100	105	
ttt tac ctt tta aac atc cgg ctg cct gtg aat gag aag aag aaa atc	747		
Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile			
110	115	120	
aat gtg gga att ggg gag ata aag gat atc cgg ttg gtg ggg atc cac	795		
Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His			
125	130	135	140
caa aat gga ggc ttc acc aag gtg tgg ttt gcc atg aag acc ttc ctt	843		
Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu			
145	150	155	
acg ccc agc atc ttc atc att atg gtg tgg tat tgg agg agg atc acc	891		
Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr			
160	165	170	
atg atg tcc cga ccc cca gtg ctt ctg gaa aaa gtc atc ttt gcc ctt	939		
Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu			
175	180	185	
ggg att tcc atg acc ttt atc aat atc cca gtg gaa tgg ttt tcc atc	987		
Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile			
190	195	200	
ggg ttt gac tgg acc tgg atg ctg ctg ttt ggt gac atc cga cag ggc	1035		
Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly			
205	210	215	220

atc ttc tat gcg atg ctt ctg tcc ttc tgg atc atc ttc tgt ggc gag	1083
Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu	
225 230 235	
cac atg atg gat cag cac gag cgg aac cac atc gca ggg tat tgg aag	1131
His Met Met Asp Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys	
240 245 250	
caa gtc gga ccc att gcc gtt ggc tcc ttc tgc ctc ttc ata ttt gac	1179
Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp	
255 260 265	
atg tgt gag aga ggg gta caa ctc acg aat ccc ttc tac agt atc tgg	1227
Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp	
270 275 280	
act aca gac att gga aca gag ctg gcc atg gcc ttc atc atc gtg gct	1275
Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala	
285 290 295 300	
gga atc tgc ctc tgc ctc tac ttc ctg ttt cta tgc ttc atg gta ttt	1323
Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe	
305 310 315	
cag gtg ttt cgg aac atc agt ggg aag cag tcc agc ctg cca gct atg	1371
Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met	
320 325 330	

agc aaa gtc cgg cgg cta cac tat gag ggg cta att ttt agg ttc aag 1419
 Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys

335

340

345

ttc ctc atg ctt atc acc ttg gcc tgc gct gcc atg act gtc atc ttc 1467
 Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe

350

355

360

ttc atc gtt agt cag gta acg gaa ggc cat tgg aaa tgg ggc ggc atc 1515
 Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile

365

370

375

380

aca gtc caa gtg aac agt gcc ttt ttc aca ggc atc tat ggg atg tgg 1563
 Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp

385

390

395

aat ctg tat gtc ttt gct ctg atg ttc ttg tat gca cca tcc cat aaa 1611
 Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys

400

405

410

aac tat gga gaa gac cag tcc aat gga atg caa ctc cca tgt aaa tcg 1659
 Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser

415

420

425

agg gaa gat tgt gct ttg ttt gtt tcg gaa ctt tat caa gaa ttg ttc 1707
 Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe

430

435

440

agc gct tcg aaa tat tcc ttc atc aat gac aac gca gct tct ggt att 1755

Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile
445 450 455 460

tgagtcaaca aggcaacaca tgtttatcag ctttgcatTT gcagttgtca cagtcacatt 1815

gattgtactt gtatacgcac acaaatacac tcatttagcc tttatctcaa aatgttaaT 1875

ataaggaaaa aagcgtcaac aataaatatt ctttgagtat tgtc 1919

<210> 149

<211> 183

<212> PRT

<213> Homo sapiens

<400> 149

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
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Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
20 25 30

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
35 40 45

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
50 55 60

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr

65	70	75	80
Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu			
85	90	95	
Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val			
100	105	110	
Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn			
115	120	125	
Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser			
130	135	140	
Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala			
145	150	155	160
Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe			
165	170	175	
Asp Arg His Lys Met Leu Ser			
180			

<210> 150

<211> 1562

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (120)..(668)

<400> 150

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ttgcggctgc agcgggcttg taggtgtccg gctttgctgg cccagcaagc ctgataagc 119

atg aag ctc tta tct ttg gtg gct gtg gtc ggg tgt ttg ctg gtg ccc 167

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro

1 5 10 15

cca gct gaa gcc aac aag agt tct gaa gat atc cgg tgc aaa tgc atc 215

Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile

20 25 30

tgt cca cct tat aga aac atc agt ggg cac att tac aac cag aat gta 263

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val

35 40 45

tcc cag aag gac tgc aac tgc ctg cac gtg gtg gag ccc atg cca gtg 311

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val

50 55 60

cct ggc cat gac gtg gag gcc tac tgc ctg ctg tgc gag tgc agg tac 359

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr

65 70 75 80

gag gag cgc agc acc acc acc atc aag gtc atc att gtc atc tac ctg 407
 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
 85 90 95

tcc gtg gtg ggt gcc ctg ttg ctc tac atg gcc ttc ctg atg ctg gtg 455
 Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
 100 105 110

gac cct ctg atc cga aag ccg gat gca tat act gag caa ctg cac aat 503
 Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
 115 120 125

gag gag gag aat gag gat gct cgc tct atg gca gca gct gct gca tcc 551
 Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser
 130 135 140

ctc ggg gga ccc cga gca aac aca gtc ctg gag cgt gtg gaa ggt gcc 599
 Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
 145 150 155 160

cag cag cgg tgg aag ctg cag gtg cag gag cag cgg aag aca gtc ttc 647
 Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
 165 170 175

gat cgg cac aag atg ctc agc tagatgggct ggtgtggttg ggtcaaggcc 698
 Asp Arg His Lys Met Leu Ser
 180

ccaacaccat ggctgccagc ttccaggetg gacaaagcag ggggctactt ctcccttccc 758

tcggttccag tcttcccttt aaaagcctgt ggcatttttc ctccttctcc ctaacttttag 818
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 ggacagctct gatgggagag ctgggcccc tgagcccact gggctcttcag ggtgcactgg 1238
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 gtgtccacag tcaactgagc agacggtcgg ttggaacatg agactcgagg ctgagcgtgg 1418
 atctgaacac cacagcccct gtacttgggt tgctctttgt ccctgaactt cgttgtacca 1478
 gtgcatggag agaaaatttt gtctctttgt cttagagttg tgtgtaaatc aaggaagcca 1538
 tcattaaatt gttttatttc tctc 1562

<210> 151

<211> 2815

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (192)..(2387)

<400> 151

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cagccaggtc tgtgctgccg ccctccagca tctttgcagc aggggacgag gctgtgtggg 120

aggctgtcgg ttcggaacat gtctccaccc accccaccct ctgtggctcc aggettcatt 180

ctcccccatc c atg gat aac cca ggg cct tcg ctc cgt ggt gcc ttt ggc 230

Met Asp Asn Pro Gly Pro Ser Leu Arg Gly Ala Phe Gly

1

5

10

att cta ggt gcc ttg gaa agg gac agg ctg acc cac ctg aaa cac aag 278

Ile Leu Gly Ala Leu Glu Arg Asp Arg Leu Thr His Leu Lys His Lys

15

20

25

ctg ggg agt ctg tgt tca ggc agc cag gag tca aag ctt ctc cat gcc 326

Leu Gly Ser Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala

30

35

40

45

atg gta ctc ctg gct ctg ggc cag gac acg gag gcc agg gtc tct ctg 374
Met Val Leu Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu
50 55 60

gag tcc ttg aag atg aac aca gta gcc cag ctg gta gcc cac cag tgg 422
Glu Ser Leu Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp
65 70 75

gca gac atg gag acc aca gag ggc cct gag gag cct cca gac ttg tcc 470
Ala Asp Met Glu Thr Thr Glu Gly Pro Glu Glu Pro Pro Asp Leu Ser
80 85 90

tgg acg gtg gct cgc ctg tac cac ctg ctg gct gag gag aac ctg tgt 518
Trp Thr Val Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys
95 100 105

ccg gcc tct aca agg gac atg gct tac cag gtg gcc ctt cgt gac ttt 566
Pro Ala Ser Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe
110 115 120 125

gcc tcc cag ggt gac cac cag ctg ggc caa ctc cag aat gag gcc tgg 614
Ala Ser Gln Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp
130 135 140

gat cgg tgc agt tca gat atc aag ggg gac ccc agt ggt ttc cag cca 662
Asp Arg Cys Ser Ser Asp Ile Lys Gly Asp Pro Ser Gly Phe Gln Pro
145 150 155

ctc cat tct cat cag ggt tcc ctg cag cca cct tca gca tcc cct gca 710

Leu His Ser His Gln Gly Ser Leu Gln Pro Pro Ser Ala Ser Pro Ala
160 165 170

gtg acc aga agc cag cct cgt ccc att gac aca cca gac tgg agt tgg 758
Val Thr Arg Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp
175 180 185

gga cat acg tta cac tcc acc aac agc act gcc tca ctg gcc agc cac 806
Gly His Thr Leu His Ser Thr Asn Ser Thr Ala Ser Leu Ala Ser His
190 195 200 205

cta gag atc agc cag tca ccc act ctt gcc ttt ctc tct tca cac cat 854
Leu Glu Ile Ser Gln Ser Pro Thr Leu Ala Phe Leu Ser Ser His His
210 215 220

gga acc cat ggg ccc agc aag cta tgt aac aca ccg ctg gac act cag 902
Gly Thr His Gly Pro Ser Lys Leu Cys Asn Thr Pro Leu Asp Thr Gln
225 230 235

gag cct cag ctt gtc cct gaa ggc tgc caa gaa cct gag gag ata agc 950
Glu Pro Gln Leu Val Pro Glu Gly Cys Gln Glu Pro Glu Glu Ile Ser
240 245 250

tgg cct cca tca gtg gag acc agt gtc tcc tta ggg tta cca cac gaa 998
Trp Pro Pro Ser Val Glu Thr Ser Val Ser Leu Gly Leu Pro His Glu
255 260 265

att agc gtt cca gag gtg tct cca gag gag gct tcg ccc atc ctc cct 1046
Ile Ser Val Pro Glu Val Ser Pro Glu Glu Ala Ser Pro Ile Leu Pro

270	275	280	285	
gac gcc ctg gct gct cca gac aca agt gtc cac tgt ccc att gaa tgc				1094
Asp Ala Leu Ala Ala Pro Asp Thr Ser Val His Cys Pro Ile Glu Cys				
	290	295	300	
aca gag ttg tct aca aac tcc agg tct ccc ctg acg tcc acc aca gaa				1142
Thr Glu Leu Ser Thr Asn Ser Arg Ser Pro Leu Thr Ser Thr Thr Glu				
	305	310	315	
agt gtt gga aag cag tgg cct att aca agt cag agg tca cct cag gtt				1190
Ser Val Gly Lys Gln Trp Pro Ile Thr Ser Gln Arg Ser Pro Gln Val				
	320	325	330	
cct gta gga gat gat tct ctg cag aac acc acg tca tcc agc cct cct				1238
Pro Val Gly Asp Asp Ser Leu Gln Asn Thr Thr Ser Ser Ser Pro Pro				
	335	340	345	
gcc cag cca cca tcc ctc caa gcc tcc cct aag ctg cct cct tcc cct				1286
Ala Gln Pro Pro Ser Leu Gln Ala Ser Pro Lys Leu Pro Pro Ser Pro				
350	355	360	365	
ctg tcc tct gct tcc tcc ccg agc agc tac cct gct cct cca acc tcc				1334
Leu Ser Ser Ala Ser Ser Pro Ser Ser Tyr Pro Ala Pro Pro Thr Ser				
	370	375	380	
aca tcc cct gtt ttg gac cac tca gaa aca tct gat cag aaa ttc tat				1382
Thr Ser Pro Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr				
	385	390	395	

aac ttt gtg gtt atc cat gcc agg gct gat gaa cag gtg gcc cta cgt	1430
Asn Phe Val Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg	
400 405 410	
att cgg gag aag ctg gag acc ctc ggg gta cct gac ggg gcc acc ttc	1478
Ile Arg Glu Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe	
415 420 425	
tgt gag gaa ttt cag gtg ccc ggg cgt ggt gag ctg cac tgt ctc caa	1526
Cys Glu Glu Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln	
430 435 440 445	
gat gcc atc gat cac tcg ggg ttc acg atc ctg ctc ctg act gct agc	1574
Asp Ala Ile Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser	
450 455 460	
ttt gat tgc agc ctg agc ctg cat caa atc aac cat gct ctc atg aac	1622
Phe Asp Cys Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn	
465 470 475	
agc ctt aca cag tct ggg agg cag gac tgt gtg atc ccc ctc ctc cca	1670
Ser Leu Thr Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro	
480 485 490	
ctt gag tgt tcc cag gcc cag ctc agc cca gat aca acc aga ctg ctc	1718
Leu Glu Cys Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu	
495 500 505	

cac agc att gtg tgg ctg gat gaa cac tcc cca atc ttc gcc aga aag	1766
His Ser Ile Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys	
510 515 520 525	

gtg gca aac acc ttc aag aca cag aag ctc cag gca cag cgg gta cgc	1814
Val Ala Asn Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg	
530 535 540	

tgg aag aaa gcg cag gag gcc aga acc ctc aag gag cag agc ata cag	1862
Trp Lys Lys Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln	
545 550 555	

ctg gag gca gag cgg caa aac gtg gca gcc ata tct gct gcc tac aca	1910
Leu Glu Ala Glu Arg Gln Asn Val Ala Ala Ile Ser Ala Ala Tyr Thr	
560 565 570	

gcc tat gtc cat agc tat agg gcc tgg caa gca gag atg aac aaa ctt	1958
Ala Tyr Val His Ser Tyr Arg Ala Trp Gln Ala Glu Met Asn Lys Leu	
575 580 585	

ggg gtg gct ttt ggg aag aac ttg tca ctg ggg act cca aca ccc agc	2006
Gly Val Ala Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser	
590 595 600 605	

tgg ccc gga tgt cca cag cca ata cct tct cat cct cag ggt ggt act	2054
Trp Pro Gly Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr	
610 615 620	

cca gtt ttc ccc tat tcc cca cag cct cca tcc ttc cct cag cct cca	2102
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Pro Val Phe Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro

625

630

635

tgc ttc cct cag cct cca tcc ttc cct cag cct cca tcc ttc cca ctg 2150

Cys Phe Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu

640

645

650

cct cca gtc tct tcc cca cag tcc caa tcc ttt cca tca gcc tcc tcc 2198

Pro Pro Val Ser Ser Pro Gln Ser Gln Ser Phe Pro Ser Ala Ser Ser

655

660

665

cca gcc cca cag act cca gga cct cag cct ctc att att cac cat gcc 2246

Pro Ala Pro Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala

670

675

680

685

cag atg gtt cag ctg ggt gtc aac aat cac atg tgg ggc cac aca ggg 2294

Gln Met Val Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly

690

695

700

gcc cag tca tct gat gac aag act gag tgt tgc gag aac ccc tgt atg 2342

Ala Gln Ser Ser Asp Asp Lys Thr Glu Cys Ser Glu Asn Pro Cys Met

705

710

715

ggc cct ctg act gat cag ggc gaa ccc ctt ctt gag act cca gag 2387

Gly Pro Leu Thr Asp Gln Gly Glu Pro Leu Leu Glu Thr Pro Glu

720

725

730

tgaccaggtt ggacccccacc tagatggcta gaggtagaag attggacttc acctgggtcc 2447

ttaaaatgat agtggaggaa gggaacctcg cctgggtccc cagagtagcc agaggactta 2507
 gcttgggctc ccacagtggc tattagttag acccagcttg agaccccaga ggcagggaag 2567
 accacaccta taaatcaggc ctgggaaaca tgcagaaacc ccatttgaac agactgtggg 2627
 actccaatct gaatcctcta tgtggacaga ggatgatggg gccagaggca cctctgaggt 2687
 gccctcagcg cagcctcgta aacttcattc actgtgacac atgctgttca tagggctctt 2747
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 gacaactg 2815

<210> 152

<211> 732

<212> PRT

<213> Mus musculus

<400> 152

Met Asp Asn Pro Gly Pro Ser Leu Arg Gly Ala Phe Gly Ile Leu Gly

1	5	10	15
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Ala Leu Glu Arg Asp Arg Leu Thr His Leu Lys His Lys Leu Gly Ser

20	25	30
----	----	----

Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala Met Val Leu

35	40	45
----	----	----

Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu Glu Ser Leu
50 55 60

Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp Ala Asp Met
65 70 75 80

Glu Thr Thr Glu Gly Pro Glu Glu Pro Pro Asp Leu Ser Trp Thr Val
85 90 95

Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys Pro Ala Ser
100 105 110

Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe Ala Ser Gln
115 120 125

Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp Asp Arg Cys
130 135 140

Ser Ser Asp Ile Lys Gly Asp Pro Ser Gly Phe Gln Pro Leu His Ser
145 150 155 160

His Gln Gly Ser Leu Gln Pro Pro Ser Ala Ser Pro Ala Val Thr Arg
165 170 175

Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp Gly His Thr
180 185 190

Leu His Ser Thr Asn Ser Thr Ala Ser Leu Ala Ser His Leu Glu Ile

195	200	205
Ser Gln Ser Pro Thr Leu Ala Phe Leu Ser Ser His His Gly Thr His		
210	215	220
Gly Pro Ser Lys Leu Cys Asn Thr Pro Leu Asp Thr Gln Glu Pro Gln		
225	230	235 240
Leu Val Pro Glu Gly Cys Gln Glu Pro Glu Glu Ile Ser Trp Pro Pro		
245	250	255
Ser Val Glu Thr Ser Val Ser Leu Gly Leu Pro His Glu Ile Ser Val		
260	265	270
Pro Glu Val Ser Pro Glu Glu Ala Ser Pro Ile Leu Pro Asp Ala Leu		
275	280	285
Ala Ala Pro Asp Thr Ser Val His Cys Pro Ile Glu Cys Thr Glu Leu		
290	295	300
Ser Thr Asn Ser Arg Ser Pro Leu Thr Ser Thr Thr Glu Ser Val Gly		
305	310	315 320
Lys Gln Trp Pro Ile Thr Ser Gln Arg Ser Pro Gln Val Pro Val Gly		
325	330	335
Asp Asp Ser Leu Gln Asn Thr Thr Ser Ser Ser Pro Pro Ala Gln Pro		
340	345	350

Pro Ser Leu Gln Ala Ser Pro Lys Leu Pro Pro Ser Pro Leu Ser Ser
355 360 365

Ala Ser Ser Pro Ser Ser Tyr Pro Ala Pro Pro Thr Ser Thr Ser Pro
370 375 380

Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr Asn Phe Val
385 390 395 400

Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg Ile Arg Glu
405 410 415

Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Glu
420 425 430

Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln Asp Ala Ile
435 440 445

Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser Phe Asp Cys
450 455 460

Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn Ser Leu Thr
465 470 475 480

Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro Leu Glu Cys
485 490 495

Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu His Ser Ile
500 505 510

Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys Val Ala Asn
515 520 525

Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg Trp Lys Lys
530 535 540

Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln Leu Glu Ala
545 550 555 560

Glu Arg Gln Asn Val Ala Ala Ile Ser Ala Ala Tyr Thr Ala Tyr Val
565 570 575

His Ser Tyr Arg Ala Trp Gln Ala Glu Met Asn Lys Leu Gly Val Ala
580 585 590

Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser Trp Pro Gly
595 600 605

Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr Pro Val Phe
610 615 620

Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Cys Phe Pro
625 630 635 640

Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu Pro Pro Val
645 650 655

Ser Ser Pro Gln Ser Gln Ser Phe Pro Ser Ala Ser Ser Pro Ala Pro

660

665

670

Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala Gln Met Val

675

680

685

Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly Ala Gln Ser

690

695

700

Ser Asp Asp Lys Thr Glu Cys Ser Glu Asn Pro Cys Met Gly Pro Leu

705

710

715

720

Thr Asp Gln Gly Glu Pro Leu Leu Glu Thr Pro Glu

725

730

<210> 153

<211> 2544

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (97)..(2232)

<400> 153

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agcttctgct gccggaggct gcacccacct gtgccc atg gcc tgc aca ggc cca 114

Met Ala Cys Thr Gly Pro

tca ctt cct agc gcc ttc gac att cta ggt gca gca ggc cag gac aag 162

Ser Leu Pro Ser Ala Phe Asp Ile Leu Gly Ala Ala Gly Gln Asp Lys

10

15

20

ctc ttg tat ctg aag cac aaa ctg aag acc cca cgc cca ggc tgc cag 210

Leu Leu Tyr Leu Lys His Lys Leu Lys Thr Pro Arg Pro Gly Cys Gln

25

30

35

ggg cag gac ctc ctg cat gcc atg gtt ctc ctg aag ctg ggc cag gaa 258

Gly Gln Asp Leu Leu His Ala Met Val Leu Leu Lys Leu Gly Gln Glu

40

45

50

act gag gcc agg atc tct cta gag gca ttg aag gcc gat gcg gtg gcc 306

Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu Lys Ala Asp Ala Val Ala

55

60

65

70

cgg ctg gtg gcc cgc cag tgg gct ggc gtg gac agc acc gag gac cca 354

Arg Leu Val Ala Arg Gln Trp Ala Gly Val Asp Ser Thr Glu Asp Pro

75

80

85

gag gag ccc cca gat gtg tcc tgg gct gtg gcc cgc ttg tac cac ctg 402

Glu Glu Pro Pro Asp Val Ser Trp Ala Val Ala Arg Leu Tyr His Leu

90

95

100

ctg gct gag gag aag ctg tgc ccc gcc tcg ctg cgg gac gtg gcc tac 450

Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser Leu Arg Asp Val Ala Tyr

105

110

115

cag gaa gcc gtc cgc acc ctc agc tcc agg gac gac cac cgg ctg ggg 498

Gln Glu Ala Val Arg Thr Leu Ser Ser Arg Asp Asp His Arg Leu Gly

120

125

130

gaa ctt cag gat gag gcc cga aac cgg tgt ggg tgg gac att gct ggg 546

Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys Gly Trp Asp Ile Ala Gly

135

140

145

150

gat cca ggg agc atc cgg acg ctc cag tcc aat ctg ggc tgc ctc cca 594

Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser Asn Leu Gly Cys Leu Pro

155

160

165

cca tcc tcg gct ttg ccc tct ggg acc agg agc ctc cca cgc ccc att 642

Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg Ser Leu Pro Arg Pro Ile

170

175

180

gac ggt gtt tcg gac tgg agc caa ggg tgc tcc ctg cga tcc act ggc 690

Asp Gly Val Ser Asp Trp Ser Gln Gly Cys Ser Leu Arg Ser Thr Gly

185

190

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agc cct gcc tcc ctg gcc agc aac ttg gaa atc agc cag tcc cct acc 738

Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu Ile Ser Gln Ser Pro Thr

200

205

210

atg ccc ttc ctc agc ctg cac cgc agc cca cat ggg ccc agc aag ctc 786

Met Pro Phe Leu Ser Leu His Arg Ser Pro His Gly Pro Ser Lys Leu

215

220

225

230

tgt gac gac ccc cag gcc agc ttg gtg ccc gag cct gtc ccc ggt ggc	834
Cys Asp Asp Pro Gln Ala Ser Leu Val Pro Glu Pro Val Pro Gly Gly	
235 240 245	

tgc cag gag cct gag gag atg agc tgg ccg cca tcg ggg gag att gcc	882
Cys Gln Glu Pro Glu Glu Met Ser Trp Pro Pro Ser Gly Glu Ile Ala	
250 255 260	

agc cca cca gag ctg cca agc agc cca cct cct ggg ctt ccc gaa gtg	930
Ser Pro Pro Glu Leu Pro Ser Ser Pro Pro Pro Gly Leu Pro Glu Val	
265 270 275	

gcc cca gat gca acc tcc act ggc ctc cct gat acc ccc gca gct cca	978
Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro Asp Thr Pro Ala Ala Pro	
280 285 290	

gaa acc agc acc aac tac cca gtg gag tgc acc gag ggg tct gca ggc	1026
Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys Thr Glu Gly Ser Ala Gly	
295 300 305 310	

ccc cag tct ctc ccc ttg cct att ctg gag ccg gtc aaa aac ccc tgc	1074
Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu Pro Val Lys Asn Pro Cys	
315 320 325	

tct gtc aaa gac cag acg cca ctc caa ctt tct gta gaa gat acc acc	1122
Ser Val Lys Asp Gln Thr Pro Leu Gln Leu Ser Val Glu Asp Thr Thr	
330 335 340	

tct cca aat acc aag ccg tgc cca cct act ccc acc acc cca gaa aca	1170
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Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr Pro Thr Thr Pro Glu Thr

345

350

355

tcc cct cct cct cct cct cct cct cct tca tct act cct tgt tca gct 1218

Ser Pro Pro Pro Pro Pro Pro Pro Pro Ser Ser Thr Pro Cys Ser Ala

360

365

370

cac ctg acc ccc tcc tcc ctg ttc cct tcc tcc ctg gaa tca tca tcg 1266

His Leu Thr Pro Ser Ser Leu Phe Pro Ser Ser Leu Glu Ser Ser Ser

375

380

385

390

gaa cag aaa ttc tat aac ttt gtg atc ctc cac gcc agg gca gac gaa 1314

Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu His Ala Arg Ala Asp Glu

395

400

405

cac atc gcc ctg cgg gtt cgg gag aag ctg gag gcc ctt ggc gtg ccc 1362

His Ile Ala Leu Arg Val Arg Glu Lys Leu Glu Ala Leu Gly Val Pro

410

415

420

gac ggg gcc acc ttc tgc gag gat ttc cag gtg ccg ggg cgc ggg gag 1410

Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln Val Pro Gly Arg Gly Glu

425

430

435

ctg agc tgc ctg cag gac gcc ata gac cac tca gct ttc atc atc cta 1458

Leu Ser Cys Leu Gln Asp Ala Ile Asp His Ser Ala Phe Ile Ile Leu

440

445

450

ctt ctc acc tcc aac ttc gac tgt cgc ctg agc ctg cac cag gtg aac 1506

Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu Ser Leu His Gln Val Asn

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caa gcc atg atg agc aac ctc acg cga cag ggg tcg cca gac tgt gtc				1554
Gln Ala Met Met Ser Asn Leu Thr Arg Gln Gly Ser Pro Asp Cys Val				
	475	480	485	
atc ccc ttc ctg ccc ctg gag agc tcc ccg gcc cag ctc agc tcc gac				1602
Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro Ala Gln Leu Ser Ser Asp				
	490	495	500	
acg gcc agc ctg ctc tcc ggg ctg gtg cgg ctg gac gaa cac tcc cag				1650
Thr Ala Ser Leu Leu Ser Gly Leu Val Arg Leu Asp Glu His Ser Gln				
	505	510	515	
atc ttc gcc agg aag gtg gcc aac acc ttc aag ccc cac agg ctt cag				1698
Ile Phe Ala Arg Lys Val Ala Asn Thr Phe Lys Pro His Arg Leu Gln				
	520	525	530	
gcc cga aag gcc atg tgg agg aag gaa cag gac acc cga gcc ctg cgg				1746
Ala Arg Lys Ala Met Trp Arg Lys Glu Gln Asp Thr Arg Ala Leu Arg				
535	540	545	550	
gaa cag agc caa cac ctg gac ggt gag cgg atg cag gcg gcg gca ctg				1794
Glu Gln Ser Gln His Leu Asp Gly Glu Arg Met Gln Ala Ala Ala Leu				
	555	560	565	
aac gca gcc tac tca gcc tac ctc cag agc tac ttg tcc tac cag gca				1842
Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser Tyr Leu Ser Tyr Gln Ala				
	570	575	580	

cag atg gag cag ctc cag gtg gct ttt ggg agc cac atg tca ttt ggg 1890
 Gln Met Glu Gln Leu Gln Val Ala Phe Gly Ser His Met Ser Phe Gly

585

590

595

act ggg gcg ccc tat ggg gct cga atg ccc ttt ggg ggc cag gtg ccc 1938
 Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro Phe Gly Gly Gln Val Pro

600

605

610

ctg gga gcc ccg cca ccc ttt ccc act tgg ccg ggg tgc ccg cag ccg 1986
 Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp Pro Gly Cys Pro Gln Pro

615

620

625

630

cca ccc ctg cac gca tgg cag gct ggc acc ccc cca ccg ccc tcc cca 2034
 Pro Pro Leu His Ala Trp Gln Ala Gly Thr Pro Pro Pro Pro Ser Pro

635

640

645

cag cca gca gcc ttt cca cag tca ctg ccc ttc ccg cag tcc cca gcc 2082
 Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro Phe Pro Gln Ser Pro Ala

650

655

660

ttc cct acg gcc tca ccc gca ccc cct cag agc cca ggg ctg caa ccc 2130
 Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln Ser Pro Gly Leu Gln Pro

665

670

675

ctc att atc cac cac gca cag atg gta cag ctg ggg ctg aac aac cac 2178
 Leu Ile Ile His His Ala Gln Met Val Gln Leu Gly Leu Asn Asn His

680

685

690

atg tgg aac cag aga ggg tcc cag gcg ccc gag gac aag acg cag gag 2226
 Met Trp Asn Gln Arg Gly Ser Gln Ala Pro Glu Asp Lys Thr Gln Glu
 695 700 705 710

gca gaa tgaccgcgtg tccttgcctg accacctggg gaacaccct ggaccaggc 2282
 Ala Glu

atcgccagg accccataga gcaccccggt ctgccctgtg ccctgtggac agtggaagat 2342

gaggtcatct gccactttca ggacattgtc cgggagccct tcatttagga caaaacgggc 2402

gcgatgatgc cctggctttc aggggtgtca gaactggata cgggtgtttac aattccaatc 2462

tctctatttc tgggtgaagg gtcttggtgg tgggggtatt gctacggtct ttttaattata 2522

ataaatattt attgaatgct tc 2544

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<211> 712

<212> PRT

<213> Homo sapiens

<400> 154

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20 25 30

Pro Arg Pro Gly Cys Gln Gly Gln Asp Leu Leu His Ala Met Val Leu
35 40 45

Leu Lys Leu Gly Gln Glu Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu
50 55 60

Lys Ala Asp Ala Val Ala Arg Leu Val Ala Arg Gln Trp Ala Gly Val
65 70 75 80

Asp Ser Thr Glu Asp Pro Glu Glu Pro Pro Asp Val Ser Trp Ala Val
85 90 95

Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser
100 105 110

Leu Arg Asp Val Ala Tyr Gln Glu Ala Val Arg Thr Leu Ser Ser Arg
115 120 125

Asp Asp His Arg Leu Gly Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys
130 135 140

Gly Trp Asp Ile Ala Gly Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser
145 150 155 160

Asn Leu Gly Cys Leu Pro Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg
165 170 175

Ser Leu Pro Arg Pro Ile Asp Gly Val Ser Asp Trp Ser Gln Gly Cys

	180		185		190										
Ser	Leu	Arg	Ser	Thr	Gly	Ser	Pro	Ala	Ser	Leu	Ala	Ser	Asn	Leu	Glu
	195					200						205			
Ile	Ser	Gln	Ser	Pro	Thr	Met	Pro	Phe	Leu	Ser	Leu	His	Arg	Ser	Pro
	210					215						220			
His	Gly	Pro	Ser	Lys	Leu	Cys	Asp	Asp	Pro	Gln	Ala	Ser	Leu	Val	Pro
225					230					235					240
Glu	Pro	Val	Pro	Gly	Gly	Cys	Gln	Glu	Pro	Glu	Glu	Met	Ser	Trp	Pro
				245					250					255	
Pro	Ser	Gly	Glu	Ile	Ala	Ser	Pro	Pro	Glu	Leu	Pro	Ser	Ser	Pro	Pro
			260						265					270	
Pro	Gly	Leu	Pro	Glu	Val	Ala	Pro	Asp	Ala	Thr	Ser	Thr	Gly	Leu	Pro
	275						280						285		
Asp	Thr	Pro	Ala	Ala	Pro	Glu	Thr	Ser	Thr	Asn	Tyr	Pro	Val	Glu	Cys
	290					295					300				
Thr	Glu	Gly	Ser	Ala	Gly	Pro	Gln	Ser	Leu	Pro	Leu	Pro	Ile	Leu	Glu
305					310					315				320	
Pro	Val	Lys	Asn	Pro	Cys	Ser	Val	Lys	Asp	Gln	Thr	Pro	Leu	Gln	Leu
				325					330					335	

Ser Val Glu Asp Thr Thr Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr
340 345 350

Pro Thr Thr Pro Glu Thr Ser Pro Pro Pro Pro Pro Pro Pro Ser
355 360 365

Ser Thr Pro Cys Ser Ala His Leu Thr Pro Ser Ser Leu Phe Pro Ser
370 375 380

Ser Leu Glu Ser Ser Ser Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu
385 390 395 400

His Ala Arg Ala Asp Glu His Ile Ala Leu Arg Val Arg Glu Lys Leu
405 410 415

Glu Ala Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln
420 425 430

Val Pro Gly Arg Gly Glu Leu Ser Cys Leu Gln Asp Ala Ile Asp His
435 440 445

Ser Ala Phe Ile Ile Leu Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu
450 455 460

Ser Leu His Gln Val Asn Gln Ala Met Met Ser Asn Leu Thr Arg Gln
465 470 475 480

Gly Ser Pro Asp Cys Val Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro
485 490 495

Ala Gln Leu Ser Ser Asp Thr Ala Ser Leu Leu Ser Gly Leu Val Arg
500 505 510

Leu Asp Glu His Ser Gln Ile Phe Ala Arg Lys Val Ala Asn Thr Phe
515 520 525

Lys Pro His Arg Leu Gln Ala Arg Lys Ala Met Trp Arg Lys Glu Gln
530 535 540

Asp Thr Arg Ala Leu Arg Glu Gln Ser Gln His Leu Asp Gly Glu Arg
545 550 555 560

Met Gln Ala Ala Ala Leu Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser
565 570 575

Tyr Leu Ser Tyr Gln Ala Gln Met Glu Gln Leu Gln Val Ala Phe Gly
580 585 590

Ser His Met Ser Phe Gly Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro
595 600 605

Phe Gly Gly Gln Val Pro Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp
610 615 620

Pro Gly Cys Pro Gln Pro Pro Pro Leu His Ala Trp Gln Ala Gly Thr
625 630 635 640

Pro Pro Pro Pro Ser Pro Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro
570/754

	645		650		655										
Phe	Pro	Gln	Ser	Pro	Ala	Phe	Pro	Thr	Ala	Ser	Pro	Ala	Pro	Pro	Gln
	660				665						670				

Ser	Pro	Gly	Leu	Gln	Pro	Leu	Ile	Ile	His	His	Ala	Gln	Met	Val	Gln
	675				680						685				

Leu	Gly	Leu	Asn	Asn	His	Met	Trp	Asn	Gln	Arg	Gly	Ser	Gln	Ala	Pro
	690				695						700				

Glu	Asp	Lys	Thr	Gln	Glu	Ala	Glu
705					710		

<210> 155

<211> 3456

<212> DNA

<213> Homo sapiens

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<221> CDS

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ggaggagagc tctgtggatg gcaaagggga ccggaagagc acaggcctga aactctccaa 180

gaagaaagca aggaggagac acacggatga cccaagcaag gaatgcttca ctctgaaatt 240

tgacctgaat gtggacattg agacagagat cgtcccagcc atg aag aag aag tca 295

Met Lys Lys Lys Ser

1

5

ctg ggg gag gtg ctg ctg cct gta ttt gaa agg aag ggc att gcg ctg 343

Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu

10

15

20

ggc aaa gtg gac atc tac ctg gac cag tcc aac aca ccc ctg tcc ctc 391

Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu

25

30

35

acc ttc gag gcc tac agg ttc ggg gga cac tac ctt cgt gtc aaa gcc 439

Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg Val Lys Ala

40

45

50

cca gcc aag cct gga gat gag ggc aag gtg gag cag ggc atg aag gac 487

Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp

55

60

65

tcc aag tcc ctg agt ttg ccg att ctg cgg cca gct ggg acc ggg ccc 535

Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro Ala Gly Thr Gly Pro

70

75

80

85

ccc gcc ctg gag cgt gtg gac gcc cag agc cgc cgg gag agc ctg gac 583

Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp
90 95 100

atc ttg gcc cct ggc cgc cgc cgc aag aac atg tcg gag ttc ctg ggg 631
Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly
105 110 115

gag gcg agc atc ccc ggg cag gag ccc ccc acg ccc tcc agc tgc tct 679
Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser Ser Cys Ser
120 125 130

ctg ccc agc ggc agc agt ggc agc acc aac act ggc gac agc tgg aag 727
Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp Ser Trp Lys
135 140 145

aac cgg gcg gcc agt cgc ttc agc ggc ttt ttc agc tcc ggc ccc agc 775
Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser
150 155 160 165

acc agc gcc ttt ggc cgg gag gta gac aag atg gag cag ctg gag ggc 823
Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met Glu Gln Leu Glu Gly
170 175 180

aag ctg cac acc tac agc ctc ttc ggg ctg ccc agg ctg ccc cgg ggg 871
Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro Arg Leu Pro Arg Gly
185 190 195

ctg cgc ttc gac cat gac tcc tgg gag gag gag tac gat gaa gac gag 919
Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu Tyr Asp Glu Asp Glu

200	205	210	
gat gag gac aat gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc			967
Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu			
215	220	225	
att gat ggg cat gag aag ctg acc cgg cgg cag tgc cac cag cag gag			1015
Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln Cys His Gln Gln Glu			
230	235	240	245
gcg gtg tgg gag ctg ctg cac acg gag gcc tcc tac atc agg aaa ctg			1063
Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser Tyr Ile Arg Lys Leu			
250	255	260	
cgg gtg atc atc aac ctg ttc ttg tgc tgc ctc ctg aac ctg caa gag			1111
Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu Leu Asn Leu Gln Glu			
265	270	275	
tca ggg ctg ctg tgt gag gtg gag gcg gag cgc ctg ttc agc aac atc			1159
Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg Leu Phe Ser Asn Ile			
280	285	290	
ccg gag atc gcg cag ctg cac cgc agg ctg tgg gct agc gtg atg gcg			1207
Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp Ala Ser Val Met Ala			
295	300	305	
ccg gtg ctg gag aag gcg cgg cgc acg cga gcg ctg cta cag ccc ggg			1255
Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala Leu Leu Gln Pro Gly			
310	315	320	325

gac ttc ctc aaa ggc ttc aag atg ttc ggc tcg ctc ttc aag ccc tac 1303

Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser Leu Phe Lys Pro Tyr

330

335

340

atc cgc tac tgc atg gag gag gag ggc tgc atg gag tac atg cgc ggc 1351

Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly

345

350

355

ctg ctg cgc gac aac gac ctc ttc cgg gcc tac atc acg tgg gcg gag 1399

Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu

360

365

370

aag cac cca cag tgc cag agg ctg aag ctg agc gac atg ctg gcc aaa 1447

Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys

375

380

385

ccc cac cag cgg ctc acc aag tac ccg ctg ctg ctc aag tcg gtg ctg 1495

Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu Leu Lys Ser Val Leu

390

395

400

405

agg aag acc gag gag ccg cgc gcc aag gag gcc gtc gtc gcc atg atc 1543

Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala Val Val Ala Met Ile

410

415

420

ggc tcc gtg gag cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag 1591

Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln

425

430

435

cgg cag gag cgg cag cgg ctg gcg gcc gtg gtg agc cgc atc gac gcc 1639
 Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala
 440 445 450

tac gag gtg gtg gaa agc agc agc gac gaa gtg gac aag ctc ctg aag 1687
 Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val Asp Lys Leu Leu Lys
 455 460 465

gaa ttt ctg cac ctg gac ttg aca gcg ccc atc cct ggc gcc tcc ccg 1735
 Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile Pro Gly Ala Ser Pro
 470 475 480 485

gag gag acg cgg cag ctg ctg ctg gag ggg agc ctg agg atg aag gag 1783
 Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser Leu Arg Met Lys Glu
 490 495 500

ggg aag gac agc aag atg gat gtg tac tgc ttc ctc ttc acg gat ctg 1831
 Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu
 505 510 515

ctg ttg gtg acc aaa gca gtg aag aag gca gag agg acc agg gtc atc 1879
 Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu Arg Thr Arg Val Ile
 520 525 530

agg cca ccc ctg ctc gtg gac aag att gtg tgc cgg gag cta cgg gac 1927
 Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu Leu Arg Asp
 535 540 545

cct ggg tcc ttc ctc ctt atc tac ctg aat gag ttt cac agt gct gta 1975
 576/754

Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His Ser Ala Val
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ggg gcc tac acg ttc cag gcc agt ggc cag gcc ttg tgc cgt ggc tgg 2023
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gtg gac acc att tac aat gcc cag aac cag ctg caa cag ctg cgt gca 2071
 Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu Gln Gln Leu Arg Ala
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cag gag ccc cca ggc agt cag cag ccc ctg cag agc ctg gaa gag gag 2119
 Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu
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gag gat gag cag gag gag gaa gag gag gag gag gag gag gag gag gaa 2167
 Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu
 615 620 625

ggc gag gac agt ggc act tca gct gcc agc tcc cct acc atc atg cgg 2215
 Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser Pro Thr Ile Met Arg
 630 635 640 645

aaa agc agc ggc agc ccc gac tct cag cac tgt gcc tca gat ggc tcc 2263
 Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys Ala Ser Asp Gly Ser
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acg gag acc ctg gcc atg gtt gtg gta gag cct ggg gac acg ctg tcc 2311
 Thr Glu Thr Leu Ala Met Val Val Val Glu Pro Gly Asp Thr Leu Ser

665	670	675	
tcc ccc gag ttc gac agc ggt cct ttc agc tcc cag tct gat gag acc	2359		
Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser Gln Ser Asp Glu Thr			
680	685	690	
tct ctc agc acc act gcc tca tct gcc acg ccc acc agt gag ctg ctg	2407		
Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro Thr Ser Glu Leu Leu			
695	700	705	
ccc ctg ggt ccg gtg gac ggc cgc tcc tgc tcc atg gac tct gcc tac	2455		
Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser Met Asp Ser Ala Tyr			
710	715	720	725
ggc acc ctc tcc cca acc tcc tta caa gac ttt gtg gcc cca ggc cca	2503		
Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe Val Ala Pro Gly Pro			
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atg gca gag cta gtg cct cgg gcc cca gag tcc cca cga gtt cct tcc	2551		
Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser			
745	750	755	
cct cca ccc tcg ccc cgt ctc cgc cgc cgc acc cct gtc cag ctg ttg	2599		
Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu			
760	765	770	
agc tgc ccg ccc cac ctg ctc aag tct aag tcc gag gcc agc ctc ctc	2647		
Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu			
775	780	785	

cag ctg ctg gca ggg gct ggc acc cat ggg aca ccc tct gcc ccc agc 2695
 Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr Pro Ser Ala Pro Ser
 790 795 800 805

cgc agc ctg tca gag ctc tgc ctg gct gtt cca gcc cca ggt att agg 2743
 Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro Ala Pro Gly Ile Arg
 810 815 820

act cag ggc tcc cct cag gaa gct ggg ccc agc tgg gat tgc cga ggg 2791
 Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser Trp Asp Cys Arg Gly
 825 830 835

gcc cct agc cct ggc agc ggt cct ggg cta gtc ggc tgc ctg gcc ggg 2839
 Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val Gly Cys Leu Ala Gly
 840 845 850

gaa cct gca ggc tcc cac agg aag agg tgt gga gac ctg ccc tcg ggg 2887
 Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly Asp Leu Pro Ser Gly
 855 860 865

gcc tct ccc agg gtc cag cct gag ccc cca cca ggg gtc tct gcc cag 2935
 Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro Gly Val Ser Ala Gln
 870 875 880 885

cac agg aag ctg acc ctg gcc cag ctc tac cga atc agg acc acc ctg 2983
 His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu
 890 895 900

ctg ctt aac tcc acg ctc act gcc tcg gag gtc tgagcagagg gaggcccca 3036
Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val

905

910

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180 185 190

Arg Leu Pro Arg Gly Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu
195 200 205

Tyr Asp Glu Asp Glu Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp
210 215 220

Ser Trp Arg Glu Leu Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln
225 230 235 240

Cys His Gln Gln Glu Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser
245 250 255

Tyr Ile Arg Lys Leu Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu
260 265 270

Leu Asn Leu Gln Glu Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg
275 280 285

Leu Phe Ser Asn Ile Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp
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Ala Ser Val Met Ala Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala
305 310 315 320

Leu Leu Gln Pro Gly Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser
325 330 335

Leu Phe Lys Pro Tyr Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met

340

345

350

Glu Tyr Met Arg Gly Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr

355

360

365

Ile Thr Trp Ala Glu Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser

370

375

380

Asp Met Leu Ala Lys Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu

385

390

395

400

Leu Lys Ser Val Leu Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala

405

410

415

Val Val Ala Met Ile Gly Ser Val Glu Arg Phe Ile His His Val Asn

420

425

430

Ala Cys Met Arg Gln Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val

435

440

445

Ser Arg Ile Asp Ala Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val

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455

460

Asp Lys Leu Leu Lys Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile

465

470

475

480

Pro Gly Ala Ser Pro Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser

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Leu Arg Met Lys Glu Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe					
	500		505		510
Leu Phe Thr Asp Leu Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu					
	515		520		525
Arg Thr Arg Val Ile Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys					
	530		535		540
Arg Glu Leu Arg Asp Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu					
545		550		555	560
Phe His Ser Ala Val Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala					
	565		570		575
Leu Cys Arg Gly Trp Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu					
	580		585		590
Gln Gln Leu Arg Ala Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln					
	595		600		605
Ser Leu Glu Glu Glu Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu					
	610		615		620
Glu Glu Glu Glu Glu Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser					
625		630		635	640

Pro Thr Ile Met Arg Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys
645 650 655

Ala Ser Asp Gly Ser Thr Glu Thr Leu Ala Met Val Val Val Glu Pro
660 665 670

Gly Asp Thr Leu Ser Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser
675 680 685

Gln Ser Asp Glu Thr Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro
690 695 700

Thr Ser Glu Leu Leu Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser
705 710 715 720

Met Asp Ser Ala Tyr Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe
725 730 735

Val Ala Pro Gly Pro Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser
740 745 750

Pro Arg Val Pro Ser Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr
755 760 765

Pro Val Gln Leu Leu Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser
770 775 780

Glu Ala Ser Leu Leu Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr
785 790 795 800

Pro Ser Ala Pro Ser Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro
805 810 815

Ala Pro Gly Ile Arg Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser
820 825 830

Trp Asp Cys Arg Gly Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val
835 840 845

Gly Cys Leu Ala Gly Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly
850 855 860

Asp Leu Pro Ser Gly Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro
865 870 875 880

Gly Val Ser Ala Gln His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg
885 890 895

Ile Arg Thr Thr Leu Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val
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cgaggcctgt gacagcaagt tccacagcac c atg cat tat gat ggg cat gtc 172

Met His Tyr Asp Gly His Val

1

5

cgc ttc gac ctt ccc cca caa ggc tct gtg ctg gcc cgg aac gtg tcc 220

Arg Phe Asp Leu Pro Pro Gln Gly Ser Val Leu Ala Arg Asn Val Ser

10

15

20

acc cgg tca tgc ccg ccg cgc acc agc ccc gca gtg gac ttg gag gag 268

Thr Arg Ser Cys Pro Pro Arg Thr Ser Pro Ala Val Asp Leu Glu Glu

25

30

35

gag gag gag gag agc tct gtg gat ggc aaa ggg gac cgg aag agc aca 316

Glu Glu Glu Glu Ser Ser Val Asp Gly Lys Gly Asp Arg Lys Ser Thr

40

45

50

55

ggc ctg aaa ctc tcc aag aag aaa gca agg agg aga cac acg gat gac 364

Gly Leu Lys Leu Ser Lys Lys Lys Ala Arg Arg Arg His Thr Asp Asp

60

65

70

cca agc aag gaa tgc ttc act ctg aaa ttt gac ctg aat gtg gac att 412

Pro Ser Lys Glu Cys Phe Thr Leu Lys Phe Asp Leu Asn Val Asp Ile	
75	80
85	
gag aca gag atc gtc cca gcc atg aag aag aag tca ctg ggg gag gtg	460
Glu Thr Glu Ile Val Pro Ala Met Lys Lys Lys Ser Leu Gly Glu Val	
90	95
100	
ctg ctg cct gta ttt gaa agg aag ggc att gcg ctg ggc aaa gtg gac	508
Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu Gly Lys Val Asp	
105	110
115	
atc tac ctg gac cag tcc aac aca ccc ctg tcc ctc acc ttc gag gcc	556
Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu Thr Phe Glu Ala	
120	125
130	135
tac agg ttc ggg gga cac tac ctt cgt gtc aaa gcc cca gcc aag cct	604
Tyr Arg Phe Gly Gly His Tyr Leu Arg Val Lys Ala Pro Ala Lys Pro	
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gga gat gag ggc aag gtg gag cag ggc atg aag gac tcc aag tcc ctg	652
Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp Ser Lys Ser Leu	
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agt ttg ccg att ctg cgg cca gct ggg acc ggg ccc ccc gcc ctg gag	700
Ser Leu Pro Ile Leu Arg Pro Ala Gly Thr Gly Pro Pro Ala Leu Glu	
170	175
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cgt gtg gac gcc cag agc cgc cgg gag agc ctg gac atc ttg gcc cct	748
Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp Ile Leu Ala Pro	

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Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly Glu Ala Ser Ile			
200	205	210	215
ccc ggg cag gag ccc ccc acg ccc tcc agc tgc tct ctg ccc agc ggc	844		
Pro Gly Gln Glu Pro Pro Thr Pro Ser Ser Cys Ser Leu Pro Ser Gly			
220	225	230	
agc agt ggc agc acc aac act ggc gac agc tgg aag aac cgg gcg gcc	892		
Ser Ser Gly Ser Thr Asn Thr Gly Asp Ser Trp Lys Asn Arg Ala Ala			
235	240	245	
agt cgc ttc agc ggc ttt ttc agc tcc ggc ccc agc acc agc gcc ttt	940		
Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser Thr Ser Ala Phe			
250	255	260	
ggc cgg gag gta gac aag atg gag cag ctg gag ggc aag ctg cac acc	988		
Gly Arg Glu Val Asp Lys Met Glu Gln Leu Glu Gly Lys Leu His Thr			
265	270	275	
tac agc ctc ttc ggg ctg ccc agg ctg ccc cgg ggg ctg cgc ttc gac	1036		
Tyr Ser Leu Phe Gly Leu Pro Arg Leu Pro Arg Gly Leu Arg Phe Asp			
280	285	290	295
cat gac tcc tgg gag gag gag tac gat gaa gac gag gat gag gac aat	1084		
His Asp Ser Trp Glu Glu Glu Tyr Asp Glu Asp Glu Asp Glu Asp Asn			
300	305	310	

gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc att gat ggg cat 1132

Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu Ile Asp Gly His

315

320

325

gag aag ctg acc cgg cgg cag tgc cac cag cag gag gcg gtg tgg gag 1180

Glu Lys Leu Thr Arg Arg Gln Cys His Gln Gln Glu Ala Val Trp Glu

330

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ctg ctg cac acg gag gcc tcc tac atc agg aaa ctg cgg gtg atc atc 1228

Leu Leu His Thr Glu Ala Ser Tyr Ile Arg Lys Leu Arg Val Ile Ile

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aac ctg ttc ctg tgc tgc ctc ctg aac ctg caa gag tca ggg ctg ctg 1276

Asn Leu Phe Leu Cys Cys Leu Leu Asn Leu Gln Glu Ser Gly Leu Leu

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365

370

375

tgt gag gtg gag gcg gag cgc ctg ttc agc aac atc ccg gag atc gcg 1324

Cys Glu Val Glu Ala Glu Arg Leu Phe Ser Asn Ile Pro Glu Ile Ala

380

385

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cag ctg cac cgc agg ctg tgg gct agc gtg atg gcg ccg gtg ctg gag 1372

Gln Leu His Arg Arg Leu Trp Ala Ser Val Met Ala Pro Val Leu Glu

395

400

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aag gcg cgg cgc acg cga gcg ctg cta cag ccc ggg gac ttc ctc aaa 1420

Lys Ala Arg Arg Thr Arg Ala Leu Leu Gln Pro Gly Asp Phe Leu Lys

410

415

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ggc ttc aag atg ttc ggc tcg ctc ttc aag ccc tac atc cgc tac tgc 1468
 Gly Phe Lys Met Phe Gly Ser Leu Phe Lys Pro Tyr Ile Arg Tyr Cys
 425 430 435

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 Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly Leu Leu Arg Asp
 440 445 450 455

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 Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu Lys His Pro Gln
 460 465 470

tgc cag agg ctg aag ctg agc gac atg ctg gcc aaa ccc cac cag cgg 1612
 Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys Pro His Gln Arg
 475 480 485

ctc acc aag tac ccg ctg ctg ctc aag tcg gtg ctg agg aag acc gag 1660
 Leu Thr Lys Tyr Pro Leu Leu Leu Lys Ser Val Leu Arg Lys Thr Glu
 490 495 500

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 Glu Pro Arg Ala Lys Glu Ala Val Val Ala Met Ile Gly Ser Val Glu
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cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag cgg cag gag cgg 1756
 Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln Arg Gln Glu Arg
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cag cgg ctg gcg gcc gtg gtg agc cgc atc gac gcc tac gag gtg gtg 1804
 591/754

Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala Tyr Glu Val Val	
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Glu Ser Ser Ser Asp Glu Val Asp Lys Leu Leu Lys Glu Phe Leu His	
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Leu Asp Leu Thr Ala Pro Ile Pro Gly Ala Ser Pro Glu Glu Thr Arg	
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cag ctg ctg ctg gag ggg agc ctg agg atg aag gag ggg aag gac agc	1948
Gln Leu Leu Leu Glu Gly Ser Leu Arg Met Lys Glu Gly Lys Asp Ser	
585	590 595
aag atg gat gtg tac tgc ttc ctc ttc acg gat ctg ctg ttg gtg acc	1996
Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu Leu Leu Val Thr	
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aaa gca gtg aag aag gca gag agg acc agg gtc atc agg cca ccc ctg	2044
Lys Ala Val Lys Lys Ala Glu Arg Thr Arg Val Ile Arg Pro Pro Leu	
620	625 630
ctc gtg gac aag att gtg tgc cgg gag cta cgg gac cct ggg tcc ttc	2092
Leu Val Asp Lys Ile Val Cys Arg Glu Leu Arg Asp Pro Gly Ser Phe	
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ctc ctt atc tac ctg aat gag ttt cac agt gct gta ggg gcc tac acg	2140
Leu Leu Ile Tyr Leu Asn Glu Phe His Ser Ala Val Gly Ala Tyr Thr	

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Phe Gln Ala Ser Gly Gln Ala Leu Cys Arg Gly Trp Val Asp Thr Ile			
665	670	675	
tac aat gcc cag aac cag ctg caa cag ctg cgt gca cag gag ccc cca			2236
Tyr Asn Ala Gln Asn Gln Leu Gln Gln Leu Arg Ala Gln Glu Pro Pro			
680	685	690	695
ggc agt cag cag ccc ctg cag agc ctg gaa gag gag gag gat gag cag			2284
Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu Glu Asp Glu Gln			
	700	705	710
gag gag gaa gag gag gag gag gag gag gag gag gaa ggc gag gac agt			2332
Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gly Glu Asp Ser			
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Gly Thr Ser Ala Ala Ser Ser Pro Thr Ile Met Arg Lys Ser Ser Gly			
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Ser Pro Asp Ser Gln His Cys Ala Ser Asp Gly Ser Thr Glu Thr Leu			
745	750	755	
gcc atg gtt gtg gta gag cct ggg gac acg ctg tcc tcc ccc gag ttc			2476
Ala Met Val Val Val Glu Pro Gly Asp Thr Leu Ser Ser Pro Glu Phe			
760	765	770	775

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 Asp Ser Gly Pro Phe Ser Ser Gln Ser Asp Glu Thr Ser Leu Ser Thr
 780 785 790

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 Thr Ala Ser Ser Ala Thr Pro Thr Ser Glu Leu Leu Pro Leu Gly Pro
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gtg gac ggc cgc tcc tgc tcc atg gac tct gcc tac ggc acc ctc tcc 2620
 Val Asp Gly Arg Ser Cys Ser Met Asp Ser Ala Tyr Gly Thr Leu Ser
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cca acc tcc tta caa gac ttt gtg gcc cca ggc cca atg gca gag cta 2668
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 Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser Pro Pro Pro Ser
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ccc cgt ctc cgc cgc cgc acc cct gtc cag ctg ttg agc tgc ccg ccc 2764
 Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu Ser Cys Pro Pro
 860 865 870

cac ctg ctc aag tct aag tcc gag gcc agc ctc ctc cag ctg ctg gca 2812
 His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu Gln Leu Leu Ala
 875 880 885

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Gly Ala Gly Thr His Gly Thr Pro Ser Ala Pro Ser Arg Ser Leu Ser

890

895

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Glu Leu Cys Leu Ala Val Pro Ala Pro Gly Ile Arg Thr Gln Gly Ser

905

910

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cct cag gaa gct ggg ccc agc tgg gat tgc cga ggg gcc cct agc cct 2956

Pro Gln Glu Ala Gly Pro Ser Trp Asp Cys Arg Gly Ala Pro Ser Pro

920

925

930

935

ggc agc ggt cct ggg cta gtc ggc tgc ctg gcc ggg gaa cct gca ggc 3004

Gly Ser Gly Pro Gly Leu Val Gly Cys Leu Ala Gly Glu Pro Ala Gly

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Ser His Arg Lys Arg Cys Gly Asp Leu Pro Ser Gly Ala Ser Pro Arg

955

960

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gtc cag cct gag ccc cca cca ggg gtc tct gcc cag cac agg aag ctg 3100

Val Gln Pro Glu Pro Pro Pro Gly Val Ser Ala Gln His Arg Lys Leu

970

975

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acc ctg gcc cag ctc tac cga atc agg acc acc ctg ctg ctt aac tcc 3148

Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu Leu Leu Asn Ser

985

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acg ctc act gcc tcg gag gtc tgagcagagg gagggcccca agagtgccat 3199

Thr Leu Thr Ala Ser Glu Val

1000

1005

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Pro Ala Val Asp Leu Glu Glu Glu Glu Glu Glu Ser Ser Val Asp Gly

35

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Lys Gly Asp Arg Lys Ser Thr Gly Leu Lys Leu Ser Lys Lys Lys Ala

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Arg Arg Arg His Thr Asp Asp Pro Ser Lys Glu Cys Phe Thr Leu Lys

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Phe Asp Leu Asn Val Asp Ile Glu Thr Glu Ile Val Pro Ala Met Lys

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Lys Lys Ser Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly

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Ile Ala Leu Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro

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120

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Leu Ser Leu Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg

130

135

140

Val Lys Ala Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly

145

150

155

160

Met Lys Asp Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro Ala Gly

165

170

175

Thr Gly Pro Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu

180	185	190
Ser Leu Asp Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu		
195	200	205
Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser		
210	215	220
Ser Cys Ser Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp		
225	230	235 240
Ser Trp Lys Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser		
245	250	255
Gly Pro Ser Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met Glu Gln		
260	265	270
Leu Glu Gly Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro Arg Leu		
275	280	285
Pro Arg Gly Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu Tyr Asp		
290	295	300
Glu Asp Glu Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp Ser Trp		
305	310	315 320
Arg Glu Leu Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln Cys His		
325	330	335

Gln Gln Glu Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser Tyr Ile
340 345 350

Arg Lys Leu Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu Leu Asn
355 360 365

Leu Gln Glu Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg Leu Phe
370 375 380

Ser Asn Ile Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp Ala Ser
385 390 395 400

Val Met Ala Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala Leu Leu
405 410 415

Gln Pro Gly Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser Leu Phe
420 425 430

Lys Pro Tyr Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr
435 440 445

Met Arg Gly Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr
450 455 460

Trp Ala Glu Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser Asp Met
465 470 475 480

Leu Ala Lys Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu Leu Lys
485 490 495

Ser Val Leu Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala Val Val
500 505 510

Ala Met Ile Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys
515 520 525

Met Arg Gln Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val Ser Arg
530 535 540

Ile Asp Ala Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val Asp Lys
545 550 555 560

Leu Leu Lys Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile Pro Gly
565 570 575

Ala Ser Pro Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser Leu Arg
580 585 590

Met Lys Glu Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe
595 600 605

Thr Asp Leu Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu Arg Thr
610 615 620

Arg Val Ile Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu
625 630 635 640

Leu Arg Asp Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His
600/754

	645		650		655
Ser	Ala	Val	Gly	Ala	Tyr
Thr	Phe	Gln	Ala	Ser	Gly
Gln	Ala	Leu	Cys		
	660		665		670
Arg	Gly	Trp	Val	Asp	Thr
Ile	Tyr	Asn	Ala	Gln	Asn
Gln	Leu	Gln	Gln		
	675		680		685
Leu	Arg	Ala	Gln	Glu	Pro
Pro	Gly	Ser	Gln	Gln	Pro
Leu	Gln	Ser	Leu		
	690		695		700
Glu	Glu	Glu	Glu	Asp	Glu
Gln	Glu	Glu	Glu	Glu	Glu
Glu	Glu	Glu	Glu	Glu	Glu
	705		710		715
					720
Glu	Glu	Glu	Gly	Glu	Asp
Ser	Gly	Thr	Ser	Ala	Ala
Ser	Ser	Pro	Thr		
	725		730		735
Ile	Met	Arg	Lys	Ser	Ser
Gly	Ser	Pro	Asp	Ser	Gln
His	Cys	Ala	Ser		
	740		745		750
Asp	Gly	Ser	Thr	Glu	Thr
Leu	Ala	Met	Val	Val	Val
Glu	Pro	Gly	Asp		
	755		760		765
Thr	Leu	Ser	Ser	Pro	Glu
Phe	Asp	Ser	Gly	Pro	Phe
Ser	Ser	Gln	Ser		
	770		775		780
Asp	Glu	Thr	Ser	Leu	Ser
Thr	Thr	Ala	Ser	Ser	Ala
Thr	Pro	Thr	Ser		
	785		790		795
					800

Glu Leu Leu Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser Met Asp
805 810 815

Ser Ala Tyr Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe Val Ala
820 825 830

Pro Gly Pro Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser Pro Arg
835 840 845

Val Pro Ser Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr Pro Val
850 855 860

Gln Leu Leu Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser Glu Ala
865 870 875 880

Ser Leu Leu Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr Pro Ser
885 890 895

Ala Pro Ser Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro Ala Pro
900 905 910

Gly Ile Arg Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser Trp Asp
915 920 925

Cys Arg Gly Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val Gly Cys
930 935 940

Leu Ala Gly Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly Asp Leu
945 950 955 960

Pro Ser Gly Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro Gly Val
 965 970 975

Ser Ala Gln His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg Ile Arg
 980 985 990

Thr Thr Leu Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val
 995 1000 1005

<210> 159

<211> 3168

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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<400> 159

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cactggcgcg atgcgggccc tcctctcggc tg atg ggt tgg aag ccc agc gag 113

Met Gly Trp Lys Pro Ser Glu

1

5

gct aga ggc cag tcc caa agt ctc cag gca tca ggg ctg cag ccc agg 161

Ala Arg Gly Gln Ser Gln Ser Leu Gln Ala Ser Gly Leu Gln Pro Arg

10	15	20	
agc ctc aag gcg gcc cgg cgg gcg act gga cgg ccg gac agg tcc cga			209
Ser Leu Lys Ala Ala Arg Arg Ala Thr Gly Arg Pro Asp Arg Ser Arg			
25	30	35	
gca gcc ccg ccc aac atg gac cca gac ccc cag gcg ggc gtg cag gtg			257
Ala Ala Pro Pro Asn Met Asp Pro Asp Pro Gln Ala Gly Val Gln Val			
40	45	50	55
ggc atg cgg gtg gtg cgc ggc gtg gac tgg aag tgg ggc cag cag gac			305
Gly Met Arg Val Val Arg Gly Val Asp Trp Lys Trp Gly Gln Gln Asp			
60	65	70	
ggc ggc gag ggc ggc gtg ggc acg gtg gtg gag ctt ggc cgc cac ggc			353
Gly Gly Glu Gly Gly Val Gly Thr Val Val Glu Leu Gly Arg His Gly			
75	80	85	
agc ccc tcg aca ccc gac cgc aca gtg gtc gtg cag tgg gac cag ggc			401
Ser Pro Ser Thr Pro Asp Arg Thr Val Val Val Gln Trp Asp Gln Gly			
90	95	100	
acg cgc acc aac tac cgc gcc ggc tac cag ggc gcg cac gac ctg ctg			449
Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu			
105	110	115	
ctg tac gac aac gcc cag atc ggc gtc cgg cac ccc aac atc atc tgt			497
Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys			
120	125	130	135

gac tgc tgc aag aag cac ggg ctg cgg ggg atg cgc tgg aag tgc cgt 545
 Asp Cys Cys Lys Lys His Gly Leu Arg Gly Met Arg Trp Lys Cys Arg
 140 145 150

gtg tgc ctg gac tac gac ctc tgc acg cag tgc tac atg cac aac aag 593
 Val Cys Leu Asp Tyr Asp Leu Cys Thr Gln Cys Tyr Met His Asn Lys
 155 160 165

cat gag ctc gcc cac gcc ttc gac cgc tac gag acc gct cac tcg cgc 641
 His Glu Leu Ala His Ala Phe Asp Arg Tyr Glu Thr Ala His Ser Arg
 170 175 180

cct gtc aca ctg agt ccc cgc cag ggc ctc ccg agg atc cca cta agg 689
 Pro Val Thr Leu Ser Pro Arg Gln Gly Leu Pro Arg Ile Pro Leu Arg
 185 190 195

ggc atc ttc cag gga gcg aag gtg gtg cga ggc ccc ttc tgg gag tgg 737
 Gly Ile Phe Gln Gly Ala Lys Val Val Arg Gly Pro Phe Trp Glu Trp
 200 205 210 215

ggc tca cag gat gga ggg gaa ggg aaa ccg ggc cgt gtg gtg gac atc 785
 Gly Ser Gln Asp Gly Gly Glu Gly Lys Pro Gly Arg Val Val Asp Ile
 220 225 230

cgt ggc tgg gat gtg gag aca ggc cgg agt gtg gcc agc gtg acg tgg 833
 Arg Gly Trp Asp Val Glu Thr Gly Arg Ser Val Ala Ser Val Thr Trp
 235 240 245

gct gat ggt acc acc aat gtg tac cgt gtg ggc cac aag ggc aag gtg	881
Ala Asp Gly Thr Thr Asn Val Tyr Arg Val Gly His Lys Gly Lys Val	
250 255 260	
gac ctc aag tgt gtg ggc gag gca gcg ggc ggc ttc tac tac aag gac	929
Asp Leu Lys Cys Val Gly Glu Ala Ala Gly Gly Phe Tyr Tyr Lys Asp	
265 270 275	
cac ctc cca agg ctc ggc aag ccg gcg gag ctg cag cgc agg gtg agt	977
His Leu Pro Arg Leu Gly Lys Pro Ala Glu Leu Gln Arg Arg Val Ser	
280 285 290 295	
gct gac agc cag ccc ttc cag cac ggg gac aag gtc aag tgt ctg ctg	1025
Ala Asp Ser Gln Pro Phe Gln His Gly Asp Lys Val Lys Cys Leu Leu	
300 305 310	
gac act gat gtc ctg cgg gag atg cag gaa ggc cac ggc ggc tgg aac	1073
Asp Thr Asp Val Leu Arg Glu Met Gln Glu Gly His Gly Gly Trp Asn	
315 320 325	
ccc agg atg gcg gag ttt atc gga cag acg ggc acc gtg cat cgt atc	1121
Pro Arg Met Ala Glu Phe Ile Gly Gln Thr Gly Thr Val His Arg Ile	
330 335 340	
acg gac cgc ggg gac gtg cgc gtg cag ttc aac cac gag acg cgc tgg	1169
Thr Asp Arg Gly Asp Val Arg Val Gln Phe Asn His Glu Thr Arg Trp	
345 350 355	
acc ttc cac ccc ggg gcg ctc acc aag cac cac tcc ttc tgg gtg ggc	1217

Thr Phe His Pro Gly Ala Leu Thr Lys His His Ser Phe Trp Val Gly
 360 365 370 375

gac gtg gtc cgg gtc atc ggc gac ctt gac aca gtg aag cgg ctg cag 1265
 Asp Val Val Arg Val Ile Gly Asp Leu Asp Thr Val Lys Arg Leu Gln
 380 385 390

gct ggg cat ggc gag tgg acg gac gac atg gcc cct gcc ctg ggc cgc 1313
 Ala Gly His Gly Glu Trp Thr Asp Asp Met Ala Pro Ala Leu Gly Arg
 395 400 405

gtc ggg aag gtg gtg aaa gtg ttt gga gac ggg aac ctg cgt gta gca 1361
 Val Gly Lys Val Val Lys Val Phe Gly Asp Gly Asn Leu Arg Val Ala
 410 415 420

gtc gct ggt cag cgg tgg acc ttc agc ccc tcc tgc ctg gtg gcc tac 1409
 Val Ala Gly Gln Arg Trp Thr Phe Ser Pro Ser Cys Leu Val Ala Tyr
 425 430 435

cgg ccc gag gag gat gcc aac ctg gac gtg gcc gag cgc gcc cgg gag 1457
 Arg Pro Glu Glu Asp Ala Asn Leu Asp Val Ala Glu Arg Ala Arg Glu
 440 445 450 455

aac aaa agc tca ctg agc gtg gcc ctg gac aag ctt cgg gcc cag aag 1505
 Asn Lys Ser Ser Leu Ser Val Ala Leu Asp Lys Leu Arg Ala Gln Lys
 460 465 470

agt gac cca gag cac ccg gga agg ctg gtg gtg gag gtg gcg ctg ggt 1553
 Ser Asp Pro Glu His Pro Gly Arg Leu Val Val Glu Val Ala Leu Gly

475	480	485	
aac gca gcc cgg gct ctg gac ctg ctg cgg agg cgc cca gag caa gtg			1601
Asn Ala Ala Arg Ala Leu Asp Leu Leu Arg Arg Arg Pro Glu Gln Val			
490	495	500	
gac acc aag aac caa ggc agg acc gct ctg caa gtg gct gcc tac ctg			1649
Asp Thr Lys Asn Gln Gly Arg Thr Ala Leu Gln Val Ala Ala Tyr Leu			
505	510	515	
ggc cag gtg gag ttg ata cgg ctg ctg cta caa gcc agg gcg ggc gtg			1697
Gly Gln Val Glu Leu Ile Arg Leu Leu Leu Gln Ala Arg Ala Gly Val			
520	525	530	535
gac ctg ccg gac gac gag ggc aac acg gca ctg cac tac gcg gcc ctg			1745
Asp Leu Pro Asp Asp Glu Gly Asn Thr Ala Leu His Tyr Ala Ala Leu			
540	545	550	
ggg aac cag ccc gag gcc acc agg gtg ctc ctg agt gct ggg tgc cgg			1793
Gly Asn Gln Pro Glu Ala Thr Arg Val Leu Leu Ser Ala Gly Cys Arg			
555	560	565	
gcg gac gcc atc aac agc acc cag agc aca gca ctg cac gtg gcc gtg			1841
Ala Asp Ala Ile Asn Ser Thr Gln Ser Thr Ala Leu His Val Ala Val			
570	575	580	
cag agg ggc ttc ctg gag gtg gtg cgg gcc ctg tgt gag cgc ggc tgt			1889
Gln Arg Gly Phe Leu Glu Val Val Arg Ala Leu Cys Glu Arg Gly Cys			
585	590	595	

gac gtc aac ctg ccc gac gcc cac tcg gac acg ccc ctg cac tcc gcc	1937
Asp Val Asn Leu Pro Asp Ala His Ser Asp Thr Pro Leu His Ser Ala	
600 605 610 615	
atc tcg gcg ggc act gga gcc agc ggc att gtc gag gtc ctc acg gag	1985
Ile Ser Ala Gly Thr Gly Ala Ser Gly Ile Val Glu Val Leu Thr Glu	
620 625 630	
gtg cca aac atc gat gtt acc gcc acc aac agc cag ggt ttc acc ctg	2033
Val Pro Asn Ile Asp Val Thr Ala Thr Asn Ser Gln Gly Phe Thr Leu	
635 640 645	
ctg cac cat gcc tcc ctc aag ggt cac gcg cta gct gtg aga aag att	2081
Leu His His Ala Ser Leu Lys Gly His Ala Leu Ala Val Arg Lys Ile	
650 655 660	
ctg gct cgg gcg cgg cag ctg gtg gac gcc aag aag gag gac ggc ttc	2129
Leu Ala Arg Ala Arg Gln Leu Val Asp Ala Lys Lys Glu Asp Gly Phe	
665 670 675	
acg gcg ctg cat ctg gct gcc ctc aac aac cac cgc gag gtg gcc cag	2177
Thr Ala Leu His Leu Ala Ala Leu Asn Asn His Arg Glu Val Ala Gln	
680 685 690 695	
atc ctc atc cgg gag ggc cgc tgt gac gtg aac gtg cgc aac cgg aag	2225
Ile Leu Ile Arg Glu Gly Arg Cys Asp Val Asn Val Arg Asn Arg Lys	
700 705 710	

ctg cag tcc ccg ctg cat ctc gcc gtg caa cag gcc cac gtg ggg ctg 2273
 Leu Gln Ser Pro Leu His Leu Ala Val Gln Gln Ala His Val Gly Leu
 715 720 725

gtg ccg cta ctg gtg gac gct ggg tgc agt gtc aac gcc gag gac gag 2321
 Val Pro Leu Leu Val Asp Ala Gly Cys Ser Val Asn Ala Glu Asp Glu
 730 735 740

gag ggg gac aca gcc ctg cac gtg gcg ctg cag cgt cat cag ctg ctg 2369
 Glu Gly Asp Thr Ala Leu His Val Ala Leu Gln Arg His Gln Leu Leu
 745 750 755

ccc ctg gtg gct gat ggg gcc ggg ggg gac cca ggg ccc ttg cag ctg 2417
 Pro Leu Val Ala Asp Gly Ala Gly Gly Asp Pro Gly Pro Leu Gln Leu
 760 765 770 775

ctg tcc agg cta cag gcc tcg ggc ctc ccc ggc agc gcg gag ctg acg 2465
 Leu Ser Arg Leu Gln Ala Ser Gly Leu Pro Gly Ser Ala Glu Leu Thr
 780 785 790

gtg ggc gcg gcg gtc gcc tgc ttc ctg gcg ctg gag ggc gcc gac gtg 2513
 Val Gly Ala Ala Val Ala Cys Phe Leu Ala Leu Glu Gly Ala Asp Val
 795 800 805

agc tac acc aac cac cgc ggt cgg agc ccg ctg gac ctg gcc gcc gag 2561
 Ser Tyr Thr Asn His Arg Gly Arg Ser Pro Leu Asp Leu Ala Ala Glu
 810 815 820

ggc cgc gtg ctc aag gcc ctt cag ggc tgc gcc cag cgc ttc cgg gag 2609
 610/754

Gly Arg Val Leu Lys Ala Leu Gln Gly Cys Ala Gln Arg Phe Arg Glu
825 830 835

cgg cag gcg ggc ggg ggc gcg gcc ccg ggc ccc agg caa acg ctc ggg 2657
Arg Gln Ala Gly Gly Gly Ala Ala Pro Gly Pro Arg Gln Thr Leu Gly
840 845 850 855

acc ccc aac acc gtg acg aac ctg cac gtg ggc gcc gcg ccg ggg ccc 2705
Thr Pro Asn Thr Val Thr Asn Leu His Val Gly Ala Ala Pro Gly Pro
860 865 870

gag gcc gct gag tgc ctg gtg tgc tcc gag ctg gcg ctg ctg gtg ctg 2753
Glu Ala Ala Glu Cys Leu Val Cys Ser Glu Leu Ala Leu Leu Val Leu
875 880 885

ttc tcg ccg tgc cag cac cgc acc gtg tgt gag gag tgc gcg cgc agg 2801
Phe Ser Pro Cys Gln His Arg Thr Val Cys Glu Glu Cys Ala Arg Arg
890 895 900

atg aag aag tgc atc agg tgc cag gtg gtc gtc agc aag aaa ctg cgc 2849
Met Lys Lys Cys Ile Arg Cys Gln Val Val Val Ser Lys Lys Leu Arg
905 910 915

cca gac ggc tct gag gtg gcg agc gcc gcc ccc gcc ccc ggc ccg ccg 2897
Pro Asp Gly Ser Glu Val Ala Ser Ala Ala Pro Ala Pro Gly Pro Pro
920 925 930 935

cgc cag ctg gtg gag gag ctg cag agc cgc tac cgg cag atg gag gaa 2945
Arg Gln Leu Val Glu Glu Leu Gln Ser Arg Tyr Arg Gln Met Glu Glu

940	945	950	
cgc atc acc tgc ccc atc tgc atc gac agg cac atc cgc ctc gtg ttc			2993
Arg Ile Thr Cys Pro Ile Cys Ile Asp Arg His Ile Arg Leu Val Phe			
955	960	965	
cag tgc ggc cac ggc gca tgc gcc ccc tgc ggc tcc gcg ctc agc gcc			3041
Gln Cys Gly His Gly Ala Cys Ala Pro Cys Gly Ser Ala Leu Ser Ala			
970	975	980	
tgc ccc atc tgc cgc cag ccc atc cgc gac cgc atc cag atc ttc gtg			3089
Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val			
985	990	995	
tgagccgcgc cgtccgccgc gcccgagctg ccttcgcgtg cccccgccct gtgttttata			3149
aaaagaaaga ttctcggat			3168

<210> 160

<211> 999

<212> PRT

<213> Homo sapiens

<400> 160

Met Gly Trp Lys Pro Ser Glu Ala Arg Gly Gln Ser Gln Ser Leu Gln

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Ala Ser Gly Leu Gln Pro Arg Ser Leu Lys Ala Ala Arg Arg Ala Thr

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Gly Arg Pro Asp Arg Ser Arg Ala Ala Pro Pro Asn Met Asp Pro Asp					
	35		40		45
Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp					
	50		55		60
Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val					
	65		70		75
					80
Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val					
		85		90	
					95
Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr					
	100		105		110
Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val					
	115		120		125
Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg					
	130		135		140
Gly Met Arg Trp Lys Cys Arg Val Cys Leu Asp Tyr Asp Leu Cys Thr					
	145		150		155
					160
Gln Cys Tyr Met His Asn Lys His Glu Leu Ala His Ala Phe Asp Arg					
	165		170		175

Tyr Glu Thr Ala His Ser Arg Pro Val Thr Leu Ser Pro Arg Gln Gly
180 185 190

Leu Pro Arg Ile Pro Leu Arg Gly Ile Phe Gln Gly Ala Lys Val Val
195 200 205

Arg Gly Pro Phe Trp Glu Trp Gly Ser Gln Asp Gly Gly Glu Gly Lys
210 215 220

Pro Gly Arg Val Val Asp Ile Arg Gly Trp Asp Val Glu Thr Gly Arg
225 230 235 240

Ser Val Ala Ser Val Thr Trp Ala Asp Gly Thr Thr Asn Val Tyr Arg
245 250 255

Val Gly His Lys Gly Lys Val Asp Leu Lys Cys Val Gly Glu Ala Ala
260 265 270

Gly Gly Phe Tyr Tyr Lys Asp His Leu Pro Arg Leu Gly Lys Pro Ala
275 280 285

Glu Leu Gln Arg Arg Val Ser Ala Asp Ser Gln Pro Phe Gln His Gly
290 295 300

Asp Lys Val Lys Cys Leu Leu Asp Thr Asp Val Leu Arg Glu Met Gln
305 310 315 320

Glu Gly His Gly Gly Trp Asn Pro Arg Met Ala Glu Phe Ile Gly Gln
325 330 335

Thr Gly Thr Val His Arg Ile Thr Asp Arg Gly Asp Val Arg Val Gln
340 345 350

Phe Asn His Glu Thr Arg Trp Thr Phe His Pro Gly Ala Leu Thr Lys
355 360 365

His His Ser Phe Trp Val Gly Asp Val Val Arg Val Ile Gly Asp Leu
370 375 380

Asp Thr Val Lys Arg Leu Gln Ala Gly His Gly Glu Trp Thr Asp Asp
385 390 395 400

Met Ala Pro Ala Leu Gly Arg Val Gly Lys Val Val Lys Val Phe Gly
405 410 415

Asp Gly Asn Leu Arg Val Ala Val Ala Gly Gln Arg Trp Thr Phe Ser
420 425 430

Pro Ser Cys Leu Val Ala Tyr Arg Pro Glu Glu Asp Ala Asn Leu Asp
435 440 445

Val Ala Glu Arg Ala Arg Glu Asn Lys Ser Ser Leu Ser Val Ala Leu
450 455 460

Asp Lys Leu Arg Ala Gln Lys Ser Asp Pro Glu His Pro Gly Arg Leu
465 470 475 480

Val Val Glu Val Ala Leu Gly Asn Ala Ala Arg Ala Leu Asp Leu Leu

	485		490		495
Arg Arg Arg Pro Glu Gln Val Asp Thr Lys Asn Gln Gly Arg Thr Ala					
	500		505		510
Leu Gln Val Ala Ala Tyr Leu Gly Gln Val Glu Leu Ile Arg Leu Leu					
	515		520		525
Leu Gln Ala Arg Ala Gly Val Asp Leu Pro Asp Asp Glu Gly Asn Thr					
	530		535		540
Ala Leu His Tyr Ala Ala Leu Gly Asn Gln Pro Glu Ala Thr Arg Val					
545		550		555	560
Leu Leu Ser Ala Gly Cys Arg Ala Asp Ala Ile Asn Ser Thr Gln Ser					
	565		570		575
Thr Ala Leu His Val Ala Val Gln Arg Gly Phe Leu Glu Val Val Arg					
	580		585		590
Ala Leu Cys Glu Arg Gly Cys Asp Val Asn Leu Pro Asp Ala His Ser					
	595		600		605
Asp Thr Pro Leu His Ser Ala Ile Ser Ala Gly Thr Gly Ala Ser Gly					
	610		615		620
Ile Val Glu Val Leu Thr Glu Val Pro Asn Ile Asp Val Thr Ala Thr					
625		630		635	640

Asn Ser Gln Gly Phe Thr Leu Leu His His Ala Ser Leu Lys Gly His
645 650 655

Ala Leu Ala Val Arg Lys Ile Leu Ala Arg Ala Arg Gln Leu Val Asp
660 665 670

Ala Lys Lys Glu Asp Gly Phe Thr Ala Leu His Leu Ala Ala Leu Asn
675 680 685

Asn His Arg Glu Val Ala Gln Ile Leu Ile Arg Glu Gly Arg Cys Asp
690 695 700

Val Asn Val Arg Asn Arg Lys Leu Gln Ser Pro Leu His Leu Ala Val
705 710 715 720

Gln Gln Ala His Val Gly Leu Val Pro Leu Leu Val Asp Ala Gly Cys
725 730 735

Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala
740 745 750

Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly
755 760 765

Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu
770 775 780

Pro Gly Ser Ala Glu Leu Thr Val Gly Ala Ala Val Ala Cys Phe Leu
785 790 795 800

Ala Leu Glu Gly Ala Asp Val Ser Tyr Thr Asn His Arg Gly Arg Ser
805 810 815

Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly
820 825 830

Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro
835 840 845

Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His
850 855 860

Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser
865 870 875 880

Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val
885 890 895

Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val
900 905 910

Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala
915 920 925

Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser
930 935 940

Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp
618/754

945 950 955 960

Arg His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro

965 970 975

Cys Gly Ser Ala Leu Ser Ala Cys Pro Ile Cys Arg Gln Pro Ile Arg

980 985 990

Asp Arg Ile Gln Ile Phe Val

995

<210> 161

<211> 3168

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (93).. (3089)

<400> 161

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cactggcgcg atgcgggccg tcctctcggc tg atg ggt tgg aag ccc agc gag 113

Met Gly Trp Lys Pro Ser Glu

1

5

gct aga ggc cag tcc caa agt ctc cag gca tca ggg ctg cag ccc agg 161

619/754

Ala Arg Gly Gln Ser Gln Ser Leu Gln Ala Ser Gly Leu Gln Pro Arg
10 15 20

agc ctc aag gcg gcc cgg cgg gcg act gga cgg ccg gac agg tcc cga 209
Ser Leu Lys Ala Ala Arg Arg Ala Thr Gly Arg Pro Asp Arg Ser Arg
25 30 35

gca gcc ccg ccc aac atg gac cca gac ccc cag gcg ggc gtg cag gtg 257
Ala Ala Pro Pro Asn Met Asp Pro Asp Pro Gln Ala Gly Val Gln Val
40 45 50 55

ggc atg cgg gtg gtg cgc ggc gtg gac tgg aag tgg ggc cag cag gac 305
Gly Met Arg Val Val Arg Gly Val Asp Trp Lys Trp Gly Gln Gln Asp
60 65 70

ggc ggc gag ggc ggc gtg ggc acg gtg gtg gag ctt ggc cgc cac ggc 353
Gly Gly Glu Gly Gly Val Gly Thr Val Val Glu Leu Gly Arg His Gly
75 80 85

agc ccc tcg aca ccc gac cgc aca gtg gtc gtg cag tgg gac cag ggc 401
Ser Pro Ser Thr Pro Asp Arg Thr Val Val Val Gln Trp Asp Gln Gly
90 95 100

acg cgc acc aac tac cgc gcc ggc tac cag ggc gcg cac gac ctg ctg 449
Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu
105 110 115

ctg tac gac aac gcc cag atc ggc gtc cgg cac ccc aac atc atc tgt 497
Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys

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Asp Cys Cys Lys Lys His Gly Leu Arg Gly Met Arg Trp Lys Cys Arg				
	140	145	150	
gtg tgc ctg gac tac gac ctc tgc acg cag tgc tac atg cac aac aag				593
Val Cys Leu Asp Tyr Asp Leu Cys Thr Gln Cys Tyr Met His Asn Lys				
	155	160	165	
cat gag ctc gcc cac gcc ttc gac cgc tac gag acc gct cac tcg cgc				641
His Glu Leu Ala His Ala Phe Asp Arg Tyr Glu Thr Ala His Ser Arg				
	170	175	180	
cct gtc aca ctg agt ccc cgc cag ggc ctc ccg agg atc cca cta agg				689
Pro Val Thr Leu Ser Pro Arg Gln Gly Leu Pro Arg Ile Pro Leu Arg				
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ggc atc ttc cag gga gcg aag gtg gtg cga ggc ccc ttc tgg gag tgg				737
Gly Ile Phe Gln Gly Ala Lys Val Val Arg Gly Pro Phe Trp Glu Trp				
200	205	210	215	
ggc tca cag gat gga ggg gaa ggg aaa ccg ggc cgt gtg gtg gac atc				785
Gly Ser Gln Asp Gly Gly Glu Gly Lys Pro Gly Arg Val Val Asp Ile				
	220	225	230	
cgt ggc tgg gat gtg gag aca ggc cgg agt gtg gcc agc gtg acg tgg				833
Arg Gly Trp Asp Val Glu Thr Gly Arg Ser Val Ala Ser Val Thr Trp				
	235	240	245	

gct gat ggt acc acc aat gtg tac cgt gtg ggc cac aag ggc aag gtg	881
Ala Asp Gly Thr Thr Asn Val Tyr Arg Val Gly His Lys Gly Lys Val	
250 255 260	
gac ctc aag tgt gtg ggc gag gca gcg ggc ggc ttc tac tac aag gac	929
Asp Leu Lys Cys Val Gly Glu Ala Ala Gly Gly Phe Tyr Tyr Lys Asp	
265 270 275	
cac ctc cca agg ctc ggc aag ccg gcg gag ctg cag cgc agg gtg agt	977
His Leu Pro Arg Leu Gly Lys Pro Ala Glu Leu Gln Arg Arg Val Ser	
280 285 290 295	
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Ala Asp Ser Gln Pro Phe Gln His Gly Asp Lys Val Lys Cys Leu Leu	
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gac act gat gtc ctg cgg gag atg cag gaa ggc cac ggc ggc tgg aac	1073
Asp Thr Asp Val Leu Arg Glu Met Gln Glu Gly His Gly Gly Trp Asn	
315 320 325	
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Pro Arg Met Ala Glu Phe Ile Gly Gln Thr Gly Thr Val His Arg Ile	
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acg gac cgc ggg gac gtg cgc gtg cag ttc aac cac gag acg cgc tgg	1169
Thr Asp Arg Gly Asp Val Arg Val Gln Phe Asn His Glu Thr Arg Trp	
345 350 355	

acc ttc cac ccc ggg gcg ctc acc aag cac cac tcc ttc tgg gtg ggc 1217
 Thr Phe His Pro Gly Ala Leu Thr Lys His His Ser Phe Trp Val Gly
 360 365 370 375

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 Asp Val Val Arg Val Ile Gly Asp Leu Asp Thr Val Lys Arg Leu Gln
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gct ggg cat ggc gag tgg acg gac gac atg gcc cct gcc ctg ggc cgc 1313
 Ala Gly His Gly Glu Trp Thr Asp Asp Met Ala Pro Ala Leu Gly Arg
 395 400 405

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 Val Gly Lys Val Val Lys Val Phe Gly Asp Gly Asn Leu Arg Val Ala
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 Val Ala Gly Gln Arg Trp Thr Phe Ser Pro Ser Cys Leu Val Ala Tyr
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cgg ccc gag gag gat gcc aac ctg gac gtg gcc gag cgc gcc cgg gag 1457
 Arg Pro Glu Glu Asp Ala Asn Leu Asp Val Ala Glu Arg Ala Arg Glu
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 Asn Lys Ser Ser Leu Ser Val Ala Leu Asp Lys Leu Arg Ala Gln Lys
 460 465 470

agt gac cca gag cac ccg gga agg ctg gtg gtg gag gtg gcg ctg ggt 1553

Ser Asp Pro Glu His Pro Gly Arg Leu Val Val Glu Val Ala Leu Gly

475

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aac gca gcc cgg gct ctg gac ctg ctg cgg agg cgc cca gag caa gtg 1601

Asn Ala Ala Arg Ala Leu Asp Leu Leu Arg Arg Arg Pro Glu Gln Val

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gac ctg ccg gac gac gag ggc aac acg gca ctg cac tac gcg gcc ctg 1745

Asp Leu Pro Asp Asp Glu Gly Asn Thr Ala Leu His Tyr Ala Ala Leu

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Gly Asn Gln Pro Glu Ala Thr Arg Val Leu Leu Ser Ala Gly Cys Arg

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gcg gac gcc atc aac agc acc cag agc aca gca ctg cac gtg gcc gtg 1841

Ala Asp Ala Ile Asn Ser Thr Gln Ser Thr Ala Leu His Val Ala Val

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cag agg ggc ttc ctg gag gtg gtg cgg gcc ctg tgt gag cgc ggc tgt 1889

Gln Arg Gly Phe Leu Glu Val Val Arg Ala Leu Cys Glu Arg Gly Cys

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gac gtc aac ctg ccc gac gcc cac tcg gac acg ccc ctg cac tcc gcc 1937
 Asp Val Asn Leu Pro Asp Ala His Ser Asp Thr Pro Leu His Ser Ala
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atc tcg gcg ggc act gga gcc agc ggc att gtc gag gtc ctc acg gag 1985
 Ile Ser Ala Gly Thr Gly Ala Ser Gly Ile Val Glu Val Leu Thr Glu
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gtg cca aac atc gat gtt acc gcc acc aac agc cag ggt ttc acc ctg 2033
 Val Pro Asn Ile Asp Val Thr Ala Thr Asn Ser Gln Gly Phe Thr Leu
 635 640 645

ctg cac cat gcc tcc ctc aag ggt cac gcg cta gct gtg aga aag att 2081
 Leu His His Ala Ser Leu Lys Gly His Ala Leu Ala Val Arg Lys Ile
 650 655 660

ctg gct cgg gcg cgg cag ctg gtg gac gcc aag aag gag gac ggc ttc 2129
 Leu Ala Arg Ala Arg Gln Leu Val Asp Ala Lys Lys Glu Asp Gly Phe
 665 670 675

acg gcg ctg cat ctg gct gcc ctc aac aac cac cgc gag gtg gcc cag 2177
 Thr Ala Leu His Leu Ala Ala Leu Asn Asn His Arg Glu Val Ala Gln
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atc ctc atc cgg gag ggc cgc tgt gac gtg aac gtg cgc aac cgg aag 2225
 Ile Leu Ile Arg Glu Gly Arg Cys Asp Val Asn Val Arg Asn Arg Lys
 700 705 710

ctg cag tcc ccg ctg cat ctc gcc gtg caa cag gcc cac gtg ggg ctg 2273

Leu Gln Ser Pro Leu His Leu Ala Val Gln Gln Ala His Val Gly Leu

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gtg ccg cta ctg gtg gac gct ggg tgc agt gtc aac gcc gag gac gag 2321

Val Pro Leu Leu Val Asp Ala Gly Cys Ser Val Asn Ala Glu Asp Glu

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gag ggg gac aca gcc ctg cac gtg gcg ctg cag cgt cat cag ctg ctg 2369

Glu Gly Asp Thr Ala Leu His Val Ala Leu Gln Arg His Gln Leu Leu

745

750

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ccc ctg gtg gct gat ggg gcc ggg ggg gac cca ggg ccc ttg cag ctg 2417

Pro Leu Val Ala Asp Gly Ala Gly Gly Asp Pro Gly Pro Leu Gln Leu

760

765

770

775

ctg tcc agg cta cag gcc tcg ggc ctc ccc ggc agc gcg gag ctg acg 2465

Leu Ser Arg Leu Gln Ala Ser Gly Leu Pro Gly Ser Ala Glu Leu Thr

780

785

790

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Val Gly Ala Ala Val Ala Cys Phe Leu Ala Leu Glu Gly Ala Asp Val

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Ser Tyr Thr Asn His Arg Gly Arg Ser Pro Leu Asp Leu Ala Ala Glu

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cgg cag gcg ggc ggg ggc gcg gcc ccg ggc ccc agg caa acg ctc ggg 2657
 Arg Gln Ala Gly Gly Gly Ala Ala Pro Gly Pro Arg Gln Thr Leu Gly
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 Thr Pro Asn Thr Val Thr Asn Leu His Val Gly Ala Ala Pro Gly Pro
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 Glu Ala Ala Glu Cys Leu Val Cys Ser Glu Leu Ala Leu Leu Val Leu
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 Phe Ser Pro Cys Gln His Arg Thr Val Cys Glu Glu Cys Ala Arg Arg
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atg aag aag tgc atc agg tgc cag gtg gtc gtc agc aag aaa ctg cgc 2849
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cca gac ggc tct gag gtg gcg agc gcc gcc ccc gcc ccc ggc ccg ccg 2897
 Pro Asp Gly Ser Glu Val Ala Ser Ala Ala Pro Ala Pro Gly Pro Pro
 920 925 930 935

cgc cag ctg gtg gag gag ctg cag agc cgc tac cgg cag atg gag gaa 2945

Arg Gln Leu Val Glu Glu Leu Gln Ser Arg Tyr Arg Gln Met Glu Glu

940

945

950

cgc atc acc tgc ccc atc tgc atc gac agc cac atc cgc ctc gtg ttc 2993

Arg Ile Thr Cys Pro Ile Cys Ile Asp Ser His Ile Arg Leu Val Phe

955

960

965

cag tgc ggc cac ggc gca tgc gcc ccc tgc ggc tcc gcg ctc agc gcc 3041

Gln Cys Gly His Gly Ala Cys Ala Pro Cys Gly Ser Ala Leu Ser Ala

970

975

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Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val

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3168

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Gly Arg Pro Asp Arg Ser Arg Ala Ala Pro Pro Asn Met Asp Pro Asp
35 40 45

Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp
50 55 60

Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val
65 70 75 80

Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val
85 90 95

Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr
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Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val
115 120 125

Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg
130 135 140

Gly Met Arg Trp Lys Cys Arg Val Cys Leu Asp Tyr Asp Leu Cys Thr
145 150 155 160

Gln Cys Tyr Met His Asn Lys His Glu Leu Ala His Ala Phe Asp Arg
165 170 175

Tyr Glu Thr Ala His Ser Arg Pro Val Thr Leu Ser Pro Arg Gln Gly

180

185

190

Leu Pro Arg Ile Pro Leu Arg Gly Ile Phe Gln Gly Ala Lys Val Val

195

200

205

Arg Gly Pro Phe Trp Glu Trp Gly Ser Gln Asp Gly Gly Glu Gly Lys

210

215

220

Pro Gly Arg Val Val Asp Ile Arg Gly Trp Asp Val Glu Thr Gly Arg

225

230

235

240

Ser Val Ala Ser Val Thr Trp Ala Asp Gly Thr Thr Asn Val Tyr Arg

245

250

255

Val Gly His Lys Gly Lys Val Asp Leu Lys Cys Val Gly Glu Ala Ala

260

265

270

Gly Gly Phe Tyr Tyr Lys Asp His Leu Pro Arg Leu Gly Lys Pro Ala

275

280

285

Glu Leu Gln Arg Arg Val Ser Ala Asp Ser Gln Pro Phe Gln His Gly

290

295

300

Asp Lys Val Lys Cys Leu Leu Asp Thr Asp Val Leu Arg Glu Met Gln

305

310

315

320

Glu Gly His Gly Gly Trp Asn Pro Arg Met Ala Glu Phe Ile Gly Gln

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Thr Gly Thr Val His Arg Ile Thr Asp Arg Gly Asp Val Arg Val Gln		
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Phe Asn His Glu Thr Arg Trp Thr Phe His Pro Gly Ala Leu Thr Lys		
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His His Ser Phe Trp Val Gly Asp Val Val Arg Val Ile Gly Asp Leu		
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Asp Thr Val Lys Arg Leu Gln Ala Gly His Gly Glu Trp Thr Asp Asp		
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Met Ala Pro Ala Leu Gly Arg Val Gly Lys Val Val Lys Val Phe Gly		
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Asp Gly Asn Leu Arg Val Ala Val Ala Gly Gln Arg Trp Thr Phe Ser		
420	425	430
Pro Ser Cys Leu Val Ala Tyr Arg Pro Glu Glu Asp Ala Asn Leu Asp		
435	440	445
Val Ala Glu Arg Ala Arg Glu Asn Lys Ser Ser Leu Ser Val Ala Leu		
450	455	460
Asp Lys Leu Arg Ala Gln Lys Ser Asp Pro Glu His Pro Gly Arg Leu		
465	470	475
		480

Val Val Glu Val Ala Leu Gly Asn Ala Ala Arg Ala Leu Asp Leu Leu
485 490 495

Arg Arg Arg Pro Glu Gln Val Asp Thr Lys Asn Gln Gly Arg Thr Ala
500 505 510

Leu Gln Val Ala Ala Tyr Leu Gly Gln Val Glu Leu Ile Arg Leu Leu
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Leu Gln Ala Arg Ala Gly Val Asp Leu Pro Asp Asp Glu Gly Asn Thr
530 535 540

Ala Leu His Tyr Ala Ala Leu Gly Asn Gln Pro Glu Ala Thr Arg Val
545 550 555 560

Leu Leu Ser Ala Gly Cys Arg Ala Asp Ala Ile Asn Ser Thr Gln Ser
565 570 575

Thr Ala Leu His Val Ala Val Gln Arg Gly Phe Leu Glu Val Val Arg
580 585 590

Ala Leu Cys Glu Arg Gly Cys Asp Val Asn Leu Pro Asp Ala His Ser
595 600 605

Asp Thr Pro Leu His Ser Ala Ile Ser Ala Gly Thr Gly Ala Ser Gly
610 615 620

Ile Val Glu Val Leu Thr Glu Val Pro Asn Ile Asp Val Thr Ala Thr
625 630 635 640

Asn Ser Gln Gly Phe Thr Leu Leu His His Ala Ser Leu Lys Gly His
645 650 655

Ala Leu Ala Val Arg Lys Ile Leu Ala Arg Ala Arg Gln Leu Val Asp
660 665 670

Ala Lys Lys Glu Asp Gly Phe Thr Ala Leu His Leu Ala Ala Leu Asn
675 680 685

Asn His Arg Glu Val Ala Gln Ile Leu Ile Arg Glu Gly Arg Cys Asp
690 695 700

Val Asn Val Arg Asn Arg Lys Leu Gln Ser Pro Leu His Leu Ala Val
705 710 715 720

Gln Gln Ala His Val Gly Leu Val Pro Leu Leu Val Asp Ala Gly Cys
725 730 735

Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala
740 745 750

Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly
755 760 765

Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu
770 775 780

Pro Gly Ser Ala Glu Leu Thr Val Gly Ala Ala Val Ala Cys Phe Leu
633/754

785	790	795	800
Ala Leu Glu Gly	Ala Asp Val Ser Tyr Thr Asn His Arg Gly Arg Ser		
	805	810	815
Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly			
	820	825	830
Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro			
	835	840	845
Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His			
	850	855	860
Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser			
865	870	875	880
Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val			
	885	890	895
Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val			
	900	905	910
Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala			
	915	920	925
Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser			
	930	935	940

Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp
 945 950 955 960

Ser His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro
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Cys Gly Ser Ala Leu Ser Ala Cys Pro Ile Cys Arg Gln Pro Ile Arg
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Asp Arg Ile Gln Ile Phe Val
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Met Ile Ala Trp Arg Leu Pro Leu

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tgc gtg ctc ttg gtg gcc tcc gtc gag agc cac ctg ggg gcc ctg ggg 162
 Cys Val Leu Leu Val Ala Ser Val Glu Ser His Leu Gly Ala Leu Gly

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ccc aag aac gtc tcg cag aaa gac gcg gag ttt gag cgc acc tac gcg 210
 Pro Lys Asn Val Ser Gln Lys Asp Ala Glu Phe Glu Arg Thr Tyr Ala

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gac gac gtc aac agc gag ctg gtc aac atc tac acc ttc aac cac acc 258
 Asp Asp Val Asn Ser Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr

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 Val Thr Arg Asn Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu

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aac aag cag aaa ggg gcg cct ttg ctg ttc gtg gtc cgc cag aag gag 354
 Asn Lys Gln Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu

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gct gtt gtg tcc ttc cag gtg ccc cta atc ctt cga gga ctg tat cag 402
 Ala Val Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Leu Tyr Gln

90

95

100

cgg aag tac ctc tac caa aaa gtg gaa cga act ctg tgt cag ccc ccc 450
 Arg Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro

105

110

115

120

acc aag aat gag tct gag atc cag ttt ttc tat gtg gac gtg tct acc 498

Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser	Thr		
				125					130					135			
ctg	tca	ccc	gtc	aat	acc	act	tac	cag	ctc	cga	gtc	aac	cgt	gtg	gac	546	
Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Asn	Arg	Val	Asp		
			140					145					150				
aat	ttt	gtg	ctc	agg	act	gga	gag	ctg	ttt	acc	ttt	aat	acc	act	gca	594	
Asn	Phe	Val	Leu	Arg	Thr	Gly	Glu	Leu	Phe	Thr	Phe	Asn	Thr	Thr	Ala		
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gcc	cag	ccc	cag	tac	ttc	aaa	tac	gag	ttt	cct	gat	ggt	gtg	gac	tgc	642	
Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Asp	Gly	Val	Asp	Ser		
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Val	Ile	Val	Lys	Val	Thr	Ser	Lys	Lys	Ala	Phe	Pro	Cys	Ser	Val	Ile		
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Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr	Asp	Leu	Asp	Asn	Ser	Val		
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Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met	Thr	Lys	Lys	Ala	Ala	Ile	Thr		
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gtg	cag	cgg	aaa	gac	ttc	ccc	agc	aac	agc	ttc	tat	gtg	gtg	gtg	gta	834	
Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser	Asn	Ser	Phe	Tyr	Val	Val	Val	Val		

235	240	245	
gtg aag act gag gac cag gcc tgc gga ggg tcc ttg ccc ttc tac cct			882
Val Lys Thr Glu Asp Gln Ala Cys Gly Gly Ser Leu Pro Phe Tyr Pro			
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ttt gtg gaa gat gag cca gtg gat caa ggg cac cgt cag aaa aca ctg			930
Phe Val Glu Asp Glu Pro Val Asp Gln Gly His Arg Gln Lys Thr Leu			
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Ser Val Leu Val Ser Gln Ala Val Thr Ser Glu Ala Tyr Val Gly Gly			
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Met Leu Phe Cys Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val			
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ctg ctg gcc tgt tgg gag aac tgg agg caa agg aag aag acc ttg ctg			1074
Leu Leu Ala Cys Trp Glu Asn Trp Arg Gln Arg Lys Lys Thr Leu Leu			
315	320	325	
gtg gcc ata gac cga gcc tgc cca gaa agt ggt cac gct cgg gtc ttg			1122
Val Ala Ile Asp Arg Ala Cys Pro Glu Ser Gly His Ala Arg Val Leu			
330	335	340	
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Ala Asp Ser Phe Pro Gly Ser Ala Pro Tyr Glu Gly Tyr Asn Tyr Gly			
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Arg Ser Phe Asp Ala Val Gly Pro Arg Pro Arg Leu Asp Ser Met Ser	
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Ser Val Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp	
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Lys Asn Val Ile Arg Thr Lys Gln Tyr Leu Cys Val Ala Asp Leu Ala	
445 450 455	

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Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp	
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Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu

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Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile

490

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tgc tac tac aac ttc ctc tgt gcc cac ccg ctg ggc aac ctc agc gcc 1650

Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala

505

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520

ttc aac aac atc ctc agc aac ttg ggg tac atc ctg ctg ggg ctg ctc 1698

Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu

525

530

535

ttc ctg ctc atc atc ctg cag cga gag atc aat cat aac cgg gcc ctg 1746

Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu

540

545

550

ctg cgg aat gac ctc tat gct ctg gag tgt ggg atc ccc aaa cac ttt 1794

Leu Arg Asn Asp Leu Tyr Ala Leu Glu Cys Gly Ile Pro Lys His Phe

555

560

565

ggc ctg ttt tac gcc atg ggc aca gca ctg atg atg gag ggg cta ctt 1842

Gly Leu Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu

570

575

580

agt gcc tgt tac cac gtc tgc ccc aac tac acc aac ttc cag ttt gat 1890

Ser Ala Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp
585 590 595 600

acc tcc ttc atg tac atg att gct ggc ctc tgc atg ctg aag ctc tac 1938
Thr Ser Phe Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr
605 610 615

cag aag cgg cac cca gat atc aac gcc agt gcc tac agt gca tat gcc 1986
Gln Lys Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala
620 625 630

tgc ttg gcc atc gtc atc ttc ttc tcc gtt ctg ggc gtg gtg ttt ggc 2034
Cys Leu Ala Ile Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly
635 640 645

aaa ggg aac acg gcc ttc tgg att gtc ttc tcc gtc att cac atc atc 2082
Lys Gly Asn Thr Ala Phe Trp Ile Val Phe Ser Val Ile His Ile Ile
650 655 660

tcc acc ctg ctc ctc agc act cag ctc tat tac atg ggc cgc tgg aag 2130
Ser Thr Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys
665 670 675 680

ctg gac ttc ggg atc ttc cgc cgc atc ctc cat gtg ctc tac aca gac 2178
Leu Asp Phe Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp
685 690 695

tgc atc cgg cag tgc agc ggg ccc ctt tac acg gac cgc atg gtg ctt 2226
Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Thr Asp Arg Met Val Leu

700	705	710	
ctg gtc atg ggc aac att atc aac tgg tcg ctg gct gca tac gga ctc			2274
Leu Val Met Gly Asn Ile Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu			
715	720	725	
atc atg cgc ccc aat gac ttt gct tcc tac ttg ctg gca att ggc atc			2322
Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile			
730	735	740	
tgc aac ctg ctg ctt tat ttc gcc ttc tac atc atc atg aag ctc cgg			2370
Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg			
745	750	755	760
agc ggc gag agg atc aag ctc atc cct ctg ctt tgc atc gtc tgc acc			2418
Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr			
765	770	775	
tcc gtg gtc tgg ggc ttc gcg ctc ttc ttc ttc ttc cag gga ctg agc			2466
Ser Val Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser			
780	785	790	
acg tgg cag aaa acc ccc gca gag tcc agg gag cac aac cgc gac tgc			2514
Thr Trp Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys			
795	800	805	
atc ctc ctc gac ttc ttt gat gac cac gat atc tgg cac ttc ctg tcc			2562
Ile Leu Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser			
810	815	820	

tcc att gcc atg ttt ggg tcc ttc ctg gtt ttg ctg acg ttg gat gac 2610

Ser Ile Ala Met Phe Gly Ser Phe Leu Val Leu Leu Thr Leu Asp Asp

825

830

835

840

gac ttg gac aca gta cag cgg gac aag atc tat gtc ttc tagcagcatc 2659

Asp Leu Asp Thr Val Gln Arg Asp Lys Ile Tyr Val Phe

845

850

tgtggtccag gcttcacctc acgggcctag cgccctgcctc tgcattcacct gccagttgcc 2719

acaagaacac cacgggtgtg agtcccagct ctgctgcccga gcattggatg tcgtggcaag 2779

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cagatgcagg taggagactt tgggggctgg ccagctgggtg ccaggctttc ggtgctaagg 3259

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 agaagaggcg ggtctgggtc tttgtttctg agctttgttc tatgttcctc catgctacgg 3979
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<212> PRT

<213> Mus musculus

<400> 164

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20 25 30

Ala Glu Phe Glu Arg Thr Tyr Ala Asp Asp Val Asn Ser Glu Leu Val
35 40 45

Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly
50 55 60

Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu
65 70 75 80

Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro
85 90 95

Leu Ile Leu Arg Gly Leu Tyr Gln Arg Lys Tyr Leu Tyr Gln Lys Val
100 105 110

Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln
115 120 125

Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr
645/754

130	135	140	
Gln Leu Arg Val Asn Arg Val Asp Asn Phe Val Leu Arg Thr Gly Glu			
145	150	155	160
Leu Phe Thr Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr			
	165	170	175
Glu Phe Pro Asp Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Lys			
	180	185	190
Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro			
	195	200	205
Val Tyr Asp Leu Asp Asn Ser Val Ala Phe Ile Gly Met Tyr Gln Thr			
	210	215	220
Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser			
225	230	235	240
Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala Cys			
	245	250	255
Gly Gly Ser Leu Pro Phe Tyr Pro Phe Val Glu Asp Glu Pro Val Asp			
	260	265	270
Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val			
	275	280	285

Thr Ser Glu Ala Tyr Val Gly Gly Met Leu Phe Cys Leu Gly Ile Phe
290 295 300

Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp
305 310 315 320

Arg Gln Arg Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro
325 330 335

Glu Ser Gly His Ala Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ala
340 345 350

Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn Gly Ser Gly Ser
355 360 365

Thr Asp Gly Leu Val Glu Ser Ala Gly Ser Gly Asp Leu Ser Tyr Ser
370 375 380

Tyr Gln Gly His Asp Gln Phe Lys Arg Arg Leu Pro Ser Gly Gln Met
385 390 395 400

Arg Gln Leu Cys Ile Ala Met Asp Arg Ser Phe Asp Ala Val Gly Pro
405 410 415

Arg Pro Arg Leu Asp Ser Met Ser Ser Val Glu Glu Asp Asp Tyr Asp
420 425 430

Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile Arg Thr Lys Gln
435 440 445

Tyr Leu Cys Val Ala Asp Leu Ala Arg Lys Asp Lys Arg Val Leu Arg
450 455 460

Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr Ile Ala Val Phe
465 470 475 480

Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr Gln Thr Val Val
485 490 495

Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala
500 505 510

His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu
515 520 525

Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg
530 535 540

Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Tyr Ala Leu
545 550 555 560

Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr
565 570 575

Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro
580 585 590

Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met Ile Ala
648/754

595	600	605
Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn		
610	615	620
Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe		
625	630	635 640
Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile		
645	650	655
Val Phe Ser Val Ile His Ile Ile Ser Thr Leu Leu Leu Ser Thr Gln		
660	665	670
Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Phe Gly Ile Phe Arg Arg		
675	680	685
Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro		
690	695	700
Leu Tyr Thr Asp Arg Met Val Leu Leu Val Met Gly Asn Ile Ile Asn		
705	710	715 720
Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala		
725	730	735
Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala		
740	745	750

Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile
755 760 765

Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu
770 775 780

Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu
785 790 795 800

Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp
805 810 815

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe
820 825 830

Leu Val Leu Leu Thr Leu Asp Asp Asp Leu Asp Thr Val Gln Arg Asp
835 840 845

Lys Ile Tyr Val Phe
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<210> 165

<211> 3138

<212> DNA

<213> Homo sapiens

<220>

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<222> (84)..(2648)

<400> 165

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gccactgccg ccctgccggg gcc atg ttc gct ctg ggc ttg ccc ttc ttg gtg 113

Met Phe Ala Leu Gly Leu Pro Phe Leu Val

1

5

10

ctc ttg gtg gcc tcg gtc gag agc cat ctg ggg gtt ctg ggg ccc aag 161

Leu Leu Val Ala Ser Val Glu Ser His Leu Gly Val Leu Gly Pro Lys

15

20

25

aac gtc tcg cag aaa gac gcc gag ttt gag cgc acc tac gtg gac gag 209

Asn Val Ser Gln Lys Asp Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu

30

35

40

gtc aac agc gag ctg gtc aac atc tac acc ttc aac cat act gtg acc 257

Val Asn Ser Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr

45

50

55

cgc aac agg aca gag ggc gtg cgt gtg tct gtg aac gtc ctg aac aag 305

Arg Asn Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys

60

65

70

cag aag ggg gcg ccg ttg ctg ttt gtg gtc cgc cag aag gag gct gtg 353

Gln Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val

75

80

85

90

gtg tcc ttc cag gtg ccc cta atc ctg cga ggg atg ttt cag cgc aag 401
Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg Lys

95

100

105

tac ctc tac caa aaa gtg gaa cga acc ctg tgt cag ccc ccc acc aag 449
Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys

110

115

120

aat gag tcg gag att cag ttc ttc tac gtg gat gtg tcc acc ctg tca 497
Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser Thr Leu Ser

125

130

135

cca gtc aac acc aca tac cag ctc cgg gtc agc cgc atg gac gat ttt 545
Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg Met Asp Asp Phe

140

145

150

gtg ctc agg act ggg gag cag ttc agc ttc aat acc aca gca gca cag 593
Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln

155

160

165

170

ccc cag tac ttc aag tat gag ttc cct gaa ggc gtg gac tcg gta att 641
Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu Gly Val Asp Ser Val Ile

175

180

185

gtc aag gtg acc tcc aac aag gcc ttc ccc tgc tca gtc atc tcc att 689
Val Lys Val Thr Ser Asn Lys Ala Phe Pro Cys Ser Val Ile Ser Ile

190

195

200

cag gat gtg ctg tgt cct gtc tat gac ctg gac aac aac gta gcc ttc 737

Gln Asp Val Leu Cys Pro Val Tyr Asp Leu Asp Asn Asn Val Ala Phe

205

210

215

atc ggc atg tac cag acg atg acc aag aag gcg gcc atc acc gta cag 785

Ile Gly Met Tyr Gln Thr Met Thr Lys Lys Ala Ala Ile Thr Val Gln

220

225

230

cgc aaa gac ttc ccc agc aac agc ttt tat gtg gtg gtg gtg gtg aag 833

Arg Lys Asp Phe Pro Ser Asn Ser Phe Tyr Val Val Val Val Val Lys

235

240

245

250

acc gaa gac caa gcc tgc ggg ggc tcc ctg cct ttc tac ccc ttc gca 881

Thr Glu Asp Gln Ala Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala

255

260

265

gaa gat gaa ccg gtc gat caa ggg cac cgc cag aaa acc ctg tca gtg 929

Glu Asp Glu Pro Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val

270

275

280

ctg gtg tct caa gca gtc acg tct gag gca tac gtc agt ggg atg ctc 977

Leu Val Ser Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly Met Leu

285

290

295

ttt tgc ctg ggt ata ttt ctc tcc ttt tac ctg ctg acc gtc ctc ctg 1025

Phe Cys Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu

300

305

310

gcc tgc tgg gag aac tgg agg cag aag aag aag acc ctg ctg gtg gcc 1073

Ala Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala

315	320	325	330	
att gac cga gcc tgc cca gaa agc ggt cac cct cga gtc ctg gct gat				1121
Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala Asp				
	335	340	345	
tct ttt cct ggc agt tcc cct tat gag ggt tac aac tat ggc tcc ttt				1169
Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe				
	350	355	360	
gag aat gtt tct gga tct acc gat ggt ctg gtt gac agc gct ggc act				1217
Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser Ala Gly Thr				
	365	370	375	
ggg gac ctc tct tac ggt tac cag ggg cac gac cag ttc aag cgg cgc				1265
Gly Asp Leu Ser Tyr Gly Tyr Gln Gly His Asp Gln Phe Lys Arg Arg				
	380	385	390	
ctc ccc tct ggc cag atg cgg cag ctg tgc att gcc atg ggc cgc tcc				1313
Leu Pro Ser Gly Gln Met Arg Gln Leu Cys Ile Ala Met Gly Arg Ser				
395	400	405	410	
ttt gaa cct gta ggt act cgg ccc cga gtg gac tcc atg agc tct gtg				1361
Phe Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val				
	415	420	425	
gag gag gat gac tac gac aca ttg acc gac atc gat tcc gac aag aat				1409
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn				
	430	435	440	

gtc att cgc acc aag caa tac ctc tat gtg gct gac ctg gca cgg aag 1457

Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys

445

450

455

gac aag cgt gtt ctg cgg aaa aag tac cag atc tac ttc tgg aac att 1505

Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile

460

465

470

gcc acc att gct gtc ttc tat gcc ctt cct gtg gtg cag ctg gtg atc 1553

Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu Val Ile

475

480

485

490

acc tac cag acg gtg gtg aat gtc aca ggg aat cag gac atc tgc tac 1601

Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr

495

500

505

tac aac ttc ctc tgc gcc cac cca ctg ggc aat ctc agc gcc ttc aac 1649

Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala Phe Asn

510

515

520

aac atc ctc agc aac ctg ggg tac atc ctg ctg ggg ctg ctt ttc ctg 1697

Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu

525

530

535

ctc atc atc ctg caa cgg gag atc aac cac aac cgg gcc ctg ctg cgc 1745

Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu Leu Arg

540

545

550

aat gac ctc tgt gcc ctg gaa tgt ggg atc ccc aaa cac ttt ggg ctt 1793
 Asn Asp Leu Cys Ala Leu Glu Cys Gly Ile Pro Lys His Phe Gly Leu
 555 560 565 570

ttc tac gcc atg ggc aca gcc ctg atg atg gag ggg ctg ctc agt gct 1841
 Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu Ser Ala
 575 580 585

tgc tat cat gtg tgc ccc aac tat acc aat ttc cag ttt gac aca tcg 1889
 Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser
 590 595 600

ttc atg tac atg atc gcc gga ctc tgc atg ctg aag ctc tac cag aag 1937
 Phe Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys
 605 610 615

cgg cac ccg gac atc aac gcc agc gcc tac agt gcc tac gcc tgc ctg 1985
 Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu
 620 625 630

gcc att gtc atc ttc ttc tct gtg ctg ggc gtg gtc ttt ggc aaa ggg 2033
 Ala Ile Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly
 635 640 645 650

aac acg gcg ttc tgg atc gtc ttc tcc atc att cac atc atc gcc acc 2081
 Asn Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr
 655 660 665

ctg ctc ctc agc acg cag ctc tat tac atg ggc cgg tgg aaa ctg gac 2129
 656/754

Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp
670 675 680

tcg ggg atc ttc cgc cgc atc ctc cac gtg ctc tac aca gac tgc atc 2177
Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp Cys Ile
685 690 695

cgg cag tgc agc ggg ccg ctc tac gtg gac cgc atg gtg ctg ctg gtc 2225
Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val Leu Leu Val
700 705 710

atg ggc aac gtc atc aac tgg tcg ctg gct gcc tat ggg ctt atc atg 2273
Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met
715 720 725 730

cgc ccc aat gat ttc gct tcc tac ttg ttg gcc att ggc atc tgc aac 2321
Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn
735 740 745

ctg ctc ctt tac ttc gcc ttc tac atc atc atg aag ctc cgg agt ggg 2369
Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly
750 755 760

gag agg atc aag ctc atc ccc ctg ctc tgc atc gtt tgc acc tcc gtg 2417
Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr Ser Val
765 770 775

gtc tgg ggc ttc gcg ctc ttc ttc ttc ttc cag gga ctc agc acc tgg 2465
Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp
657/754

780	785	790	
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Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys Ile Leu			
795	800	805	810
ctc gac ttc ttt gac gac cac gac atc tgg cac ttc ctc tcc tcc atc			2561
Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser Ser Ile			
	815	820	825
gcc atg ttc ggg tcc ttc ctg gta agc ggg cct ccc ggc cga gcc ggg			2609
Ala Met Phe Gly Ser Phe Leu Val Ser Gly Pro Pro Gly Arg Ala Gly			
	830	835	840
tgg gta cgt gaa ggt agc agc tgc ctc ctt ccc tgt ggc tgatctggcg			2658
Trp Val Arg Glu Gly Ser Ser Cys Leu Leu Pro Cys Gly			
	845	850	855
tccacacccc aggtgttgct gacactggat gacgacctgg atacttagaa aggggcttca			2718
ggaagggatg tgctgtttcc ctctacgtgc ccagtcctag cctcgctcta ggaccaggg			2778
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<210> 166

<211> 855

<212> PRT

<213> Homo sapiens

<400> 166

Met Phe Ala Leu Gly Leu Pro Phe Leu Val Leu Leu Val Ala Ser Val

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Glu Ser His Leu Gly Val Leu Gly Pro Lys Asn Val Ser Gln Lys Asp

20 25 30

Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu Val Asn Ser Glu Leu Val

35 40 45

Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly

50 55 60

Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu

65 70 75 80

Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro

85 90 95

Leu Ile Leu Arg Gly Met Phe Gln Arg Lys Tyr Leu Tyr Gln Lys Val
100 105 110

Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln
115 120 125

Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr
130 135 140

Gln Leu Arg Val Ser Arg Met Asp Asp Phe Val Leu Arg Thr Gly Glu
145 150 155 160

Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr
165 170 175

Glu Phe Pro Glu Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn
180 185 190

Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro
195 200 205

Val Tyr Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr
210 215 220

Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
225 230 235 240

Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala Cys

	245		250		255
Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro Val Asp					
	260		265		270
Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val					
	275		280		285
Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys Leu Gly Ile Phe					
	290		295		300
Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp					
305		310		315	320
Arg Gln Lys Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro					
	325		330		335
Glu Ser Gly His Pro Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ser					
	340		345		350
Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn Val Ser Gly Ser					
	355		360		365
Thr Asp Gly Leu Val Asp Ser Ala Gly Thr Gly Asp Leu Ser Tyr Gly					
	370		375		380
Tyr Gln Gly His Asp Gln Phe Lys Arg Arg Leu Pro Ser Gly Gln Met					
385		390		395	400

Arg Gln Leu Cys Ile Ala Met Gly Arg Ser Phe Glu Pro Val Gly Thr
405 410 415

Arg Pro Arg Val Asp Ser Met Ser Ser Val Glu Glu Asp Asp Tyr Asp
420 425 430

Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile Arg Thr Lys Gln
435 440 445

Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys Asp Lys Arg Val Leu Arg
450 455 460

Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr Ile Ala Val Phe
465 470 475 480

Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr Gln Thr Val Val
485 490 495

Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala
500 505 510

His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu
515 520 525

Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg
530 535 540

Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu
545 550 555 560

Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr
565 570 575

Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro
580 585 590

Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met Ile Ala
595 600 605

Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn
610 615 620

Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe
625 630 635 640

Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile
645 650 655

Val Phe Ser Ile Ile His Ile Ile Ala Thr Leu Leu Leu Ser Thr Gln
660 665 670

Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Ser Gly Ile Phe Arg Arg
675 680 685

Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro
690 695 700

Leu Tyr Val Asp Arg Met Val Leu Leu Val Met Gly Asn Val Ile Asn
663/754

705 710 715 720

Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala

725 730 735

Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala

740 745 750

Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile

755 760 765

Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu

770 775 780

Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu

785 790 795 800

Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp

805 810 815

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe

820 825 830

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835 840 845

Ser Cys Leu Leu Pro Cys Gly

850 855

<210> 167

<211> 2815

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (56).. (571)

<400> 167

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Met

1

agg cgc cag cct gcg aag gtg gcg gcg ctg ctg ctc ggg ctg ctc ttg 106

Arg Arg Gln Pro Ala Lys Val Ala Ala Leu Leu Leu Gly Leu Leu Leu

5

10

15

gag tgc aca gaa gcc aaa aag cat tgc tgg tat ttc gaa gga ctc tat 154

Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu Tyr

20

25

30

cca acc tat tat ata tgc cgc tcc tac gag gac tgc tgt ggc tcc agg 202

Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser Arg

35

40

45

tgc tgt gtg cgg gcc ctc tcc ata cag agg ctg tgg tac ttc tgg ttc 250

Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp Phe

50	55	60	65	
ctt ctg atg atg ggc gtg ctt ttc tgc tgc gga gcc ggc ttc ttc atc				298
Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe Ile				
	70	75	80	
cgg agg cgc atg tac ccc ccg ccg ctg atc gag gag cca gcc ttc aat				346
Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn				
	85	90	95	
gtg tcc tac acc agg cag ccc cca aat ccc ggc cca gga gcc cag cag				394
Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln				
	100	105	110	
ccg ggg ccg ccc tat tac acc gac cca gga gga ccg ggg atg aac cct				442
Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro				
	115	120	125	
gtc ggg aat tcc atg gca atg gct ttc cag gtc cca ccc aac tca ccc				490
Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro				
	130	135	140	145
cag ggg agt gtg gcc tgc ccg ccc cct cca gcc tac tgc aac acg cct				538
Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr Pro				
	150	155	160	
ccg ccc ccg tac gaa cag gta gtg aag gcc aag tagtggggtg cccacgtgca				591
Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys				
	165	170		

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cacattcctg gataggaatc acagctcacc ccaggatctc acaggtagtc tcctgagtag 1791

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ctgtatcacg gggaatgagg tgggggtgct tatttttttaa tgaactaatc agagcctctt 1971

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 gggc 2815

<210> 168

<211> 172

<212> PRT

<213> Homo sapiens

<400> 168

Met Arg Arg Gln Pro Ala Lys Val Ala Ala Leu Leu Leu Gly Leu Leu

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Leu Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu
20 25 30

Tyr Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser
35 40 45

Arg Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp
50 55 60

Phe Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe
65 70 75 80

Ile Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe
85 90 95

Asn Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln
100 105 110

Gln Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn
115 120 125

Pro Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser
130 135 140

Pro Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr
145 150 155 160

Pro Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys
165 170

<210> 169

<211> 3337

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (136)..(1755)

<400> 169

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tacccgagtc tcgtttcctc tcagtccatc cacccttcat ggggccagag ccctctctcc 120

agaatctgag cagca atg ccg ttt gct gaa gac aag acc tat aag tat atc 171

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile

1

5

10

tgc cgc aat ttc agc aat ttt tgc aat gtg gat gtt gta gag att ctg 219

Cys Arg Asn Phe Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu

15

20

25

cct tac ctg ccc tgc ctc aca gca aga gac cag gat cga ctg cgg gcc 267

Pro Tyr Leu Pro Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala

30

35

40

acc tgc aca ctc tca ggg aac cgg gac acc ctc tgg cat ctc ttc aat 315

Thr Cys Thr Leu Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn
 45 50 55 60

acc ctt cag cgg cgg ccc ggc tgg gtg gag tac ttc att gcg gca ctg 363
 Thr Leu Gln Arg Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu
 65 70 75

agg ggc tgt gag cta gtt gat ctc gcg gac gaa gtg gcc tct gtc tac 411
 Arg Gly Cys Glu Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr
 80 85 90

cag agc tac cag cct cgg acc tcg gac cgt ccc cca gac cca ctg gag 459
 Gln Ser Tyr Gln Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu
 95 100 105

cca ccg tca ctt cct gct gag agg cca ggg ccc ccc aca cct gct gcg 507
 Pro Pro Ser Leu Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala
 110 115 120

gcc cac agc atc ccc tac aac agc tgc aga gag aag gag cca agt tac 555
 Ala His Ser Ile Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr
 125 130 135 140

ccc atg cct gtc cag gag acc cag gcg cca gag tcc cca gga gag aat 603
 Pro Met Pro Val Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn
 145 150 155

tca gag caa gcc ctg cag acg ctc agc ccc aga gcc atc cca agg aat 651
 Ser Glu Gln Ala Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn

160	165	170	
cca gat ggt ggc ccc ctg gag tcc tcc tct gac ctg gca gcc ctc agc	699		
Pro Asp Gly Gly Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser			
175	180	185	
cct ctg acc tcc agc ggg cat cag gag cag gac aca gaa ctg ggc agt	747		
Pro Leu Thr Ser Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser			
190	195	200	
acc cac aca gca ggt gcg acc tcc agc ctc aca cca tcc cgt ggg cct	795		
Thr His Thr Ala Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro			
205	210	215	220
gtg tct cca tct gtc tcc ttc cag ccc ctg gcc cgt tcc acc ccc agg	843		
Val Ser Pro Ser Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg			
225	230	235	
gca agc cgc ttg cct gga ccc aca ggg tca gtt gta tct act ggc acc	891		
Ala Ser Arg Leu Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr			
240	245	250	
tcc ttc tcc tcc tca tcc cct ggc ttg gcc tct gca ggg gct gca gag	939		
Ser Phe Ser Ser Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu			
255	260	265	
ggt aaa cag ggt gca gag agt gac cag gcc gag cct atc atc tgc tcc	987		
Gly Lys Gln Gly Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser			
270	275	280	

agt ggg gca gag gca cct gcc aac tct ctg ccc tcc aaa gtg cct acc 1035

285 290 295 300

Thr Leu Met Pro Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro

gca tct gtc agc aca gtg ccc tcc aag ttg cca act agc tca aag ccc 1131

320 325 330

335 340 345

350 355 360

365 370 375 380

385 390 395

gcc act gga ggc agc tca gcc tgg cta gac agc agc tct gag aat agg 1371
 Ala Thr Gly Gly Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg

400

405

410

ggc ctt ggg tcg gag ctg agt aag cct ggc gtg ctg gca tcc cag gta 1419
 Gly Leu Gly Ser Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val

415

420

425

gac agc ccg ttc tcg ggc tgc ttc gag gat ctt gcc atc agt gcc agc 1467
 Asp Ser Pro Phe Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser

430

435

440

acc tcc ttg ggc atg ggg ccc tgc cat ggc cca gag gag aat gag tat 1515
 Thr Ser Leu Gly Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr

445

450

455

460

aag tcc gag ggc acc ttt ggg atc cac gtg gct gag aac ccc agc atc 1563
 Lys Ser Glu Gly Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile

465

470

475

cag ctc ctg gag ggc aac cct ggg cca cct gcg gac ccg gat ggc ggc 1611
 Gln Leu Leu Glu Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly

480

485

490

ccc agg cca caa gcc gac cgg aag ttc cag gag agg gag gtg cca tgc 1659
 Pro Arg Pro Gln Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys

495

500

505

cac agg ccc tca cct ggg gct ctg tgg ctc cag gtg gct gtg aca ggg 1707

His Arg Pro Ser Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly

510

515

520

gtg ctg gta gtc aca ctc ctg gtg gtg ctg tac cgg cgg cgt ctg cac 1755

Val Leu Val Val Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His

525

530

535

540

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atccccatcc cccaccacca atcttaaaaa gccctctgtc ccctaccct aaacccagc 3255

taggtacca tgctgggcag gtcagttaac aatttatgca caggtagtag ttttattgta 3315

ttaccgttcc agggtagctt tg

3337

<210> 170

<211> 540

<212> PRT

<213> Homo sapiens

<400> 170

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe

1 5 10 15

Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro

20 25 30

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu

35 40 45

Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg

50 55 60

Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu

65 70 75 80

Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Gln Ser Tyr Gln

85 90 95

Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu

678/754

100	105	110
Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile		
115	120	125
Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val		
130	135	140
Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala		
145	150	155
Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp Gly Gly		
165	170	175
Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu Thr Ser		
180	185	190
Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser Thr His Thr Ala		
195	200	205
Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser Pro Ser		
210	215	220
Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg Ala Ser Arg Leu		
225	230	235
Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr Ser Phe Ser Ser		
245	250	255

Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu Gly Lys Gln Gly
260 265 270

Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser Ser Gly Ala Glu
275 280 285

Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr Leu Met Pro
290 295 300

Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala Ser Val Ser
305 310 315 320

Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro Gly Ala Val
325 330 335

Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu Pro Ile Asn
340 345 350

Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser Met Val
355 360 365

Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly Ser Ser Arg
370 375 380

Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala Thr Gly Gly
385 390 395 400

Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg Gly Leu Gly Ser
405 410 415

Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser Pro Phe
420 425 430

Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser Leu Gly
435 440 445

Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser Glu Gly
450 455 460

Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln Leu Leu Glu
465 470 475 480

Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg Pro Gln
485 490 495

Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg Pro Ser
500 505 510

Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly Val Leu Val Val
515 520 525

Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His
530 535 540

<210> 171

<211> 3579

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (242).. (3094)

<400> 171

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gcggggcgcc gacgaggagt gcaggactca ggaagggcga gtgcgcggcg acagagcccc 180

gggaaggagg cagggaagg ccgggcttgg gggcaggtgg tccgggcac cagccttgaa 240

g atg cac aag agg aaa gga ccc ccg gga ccc ccg ggc aga ggc gcc gcg 289

Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala

1

5

10

15

gcc gcc cgc cag ctg ggc ctg ctg gtt gac ctc tcc cca gat ggc ctg 337

Ala Ala Arg Gln Leu Gly Leu Leu Val Asp Leu Ser Pro Asp Gly Leu

20

25

30

atg atc cct gag gac ggg gct aac gat gaa gaa ctg gag gct gag ttc 385

Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe

35

40

45

ttg gct ttg gtc ggg ggc cag ccc cca gcc ctg gag aag ctc aaa ggc 433

Leu Ala Leu Val Gly Gly Gln Pro Pro Ala Leu Glu Lys Leu Lys Gly

50	55	60	
aaa ggt ccc ttg ccg atg gag gcc att gag aag atg gcc agc ctg tgc	481		
Lys Gly Pro Leu Pro Met Glu Ala Ile Glu Lys Met Ala Ser Leu Cys			
65	70	75	80
atg aga gac ccg gat gag gat gag gag gag ggg acg gat gag gac gac	529		
Met Arg Asp Pro Asp Glu Asp Glu Glu Glu Gly Thr Asp Glu Asp Asp			
	85	90	95
ttg gag gct gat gat gac ctg ctg gcg gag cta aat gag gtc ctt gga	577		
Leu Glu Ala Asp Asp Asp Leu Leu Ala Glu Leu Asn Glu Val Leu Gly			
	100	105	110
gag gag cag aag gct tca gag acc cca cct cct gtg gcc cag ccg aag	625		
Glu Glu Gln Lys Ala Ser Glu Thr Pro Pro Pro Val Ala Gln Pro Lys			
	115	120	125
cct gag gcc cct cat ccg ggg ctg gag acc acc ttg cag gag agg ctg	673		
Pro Glu Ala Pro His Pro Gly Leu Glu Thr Thr Leu Gln Glu Arg Leu			
	130	135	140
gcg ctc tat cag aca gca att gaa agc gcc aga caa gct gga gac agc	721		
Ala Leu Tyr Gln Thr Ala Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser			
	145	150	155
gcc aag atg cgg cgc tac gat cgg ggg ctt aaa aca ctg gaa aac ctg	769		
Ala Lys Met Arg Arg Tyr Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu			
	165	170	175

ctc gcc tcc atc cgt aag ggc aat gcc att gac gaa gcg gac atc ccg 817
 Leu Ala Ser Ile Arg Lys Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro

180

185

190

ccg cca gtg gcc ata gga aaa ggc ccg gcg tcc acg cct acc tac agc 865
 Pro Pro Val Ala Ile Gly Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser

195

200

205

cct gca ccc acc cag ccg gcc cct aga atc gcg tca gcc cca gag ccc 913
 Pro Ala Pro Thr Gln Pro Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro

210

215

220

agg gtc acc ctg gag gga cct tct gcc acc gcc cca gcc tca tct cca 961
 Arg Val Thr Leu Glu Gly Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro

225

230

235

240

ggc ttg gct aag ccc cag atg ccc cca ggt ccc tgc agc cct ggc cct 1009
 Gly Leu Ala Lys Pro Gln Met Pro Pro Gly Pro Cys Ser Pro Gly Pro

245

250

255

ctg gcc cag ttg cag agc cgc cag cgc gac tac aag ctg gct gcc ctc 1057
 Leu Ala Gln Leu Gln Ser Arg Gln Arg Asp Tyr Lys Leu Ala Ala Leu

260

265

270

cac gcc aag cag cag gga gat acc act gct gcc gct aga cac ttc cgc 1105
 His Ala Lys Gln Gln Gly Asp Thr Thr Ala Ala Ala Arg His Phe Arg

275

280

285

gtg gct aag agc ttt gat gct gtc ttg gag gcc ctg agc cgg ggt gag 1153
Val Ala Lys Ser Phe Asp Ala Val Leu Glu Ala Leu Ser Arg Gly Glu
290 295 300

ccc gtg gac ctc tcc tgc ctg ccc cct cca ccc gac cag ctg ccc cca 1201
Pro Val Asp Leu Ser Cys Leu Pro Pro Pro Pro Asp Gln Leu Pro Pro
305 310 315 320

gac cca ccg tca cca ccg tgc cag cct ccg acc ccc gct acg gcg ccc 1249
Asp Pro Pro Ser Pro Pro Ser Gln Pro Pro Thr Pro Ala Thr Ala Pro
325 330 335

tcc aca aca gag gtg ccc cca ccc ccg agg acc ctg ctg gag gcg ctg 1297
Ser Thr Thr Glu Val Pro Pro Pro Pro Arg Thr Leu Leu Glu Ala Leu
340 345 350

gag cag cgg atg gag cgg tac cag gtg gcc gca gcc cag gcc aag agc 1345
Glu Gln Arg Met Glu Arg Tyr Gln Val Ala Ala Ala Gln Ala Lys Ser
355 360 365

aag ggg gac cag cgg aaa gct cga atg cac gag cgc atc gtc aag caa 1393
Lys Gly Asp Gln Arg Lys Ala Arg Met His Glu Arg Ile Val Lys Gln
370 375 380

tac caa gat gcc atc cga gcc cac aag gct ggc cga gcc gtg gat gtc 1441
Tyr Gln Asp Ala Ile Arg Ala His Lys Ala Gly Arg Ala Val Asp Val
385 390 395 400

gct gaa ttg ccc gtg ccc cca ggc ttc ccc cca atc cag ggc ctg gag 1489

Ala Glu Leu Pro Val Pro Pro Gly Phe Pro Pro Ile Gln Gly Leu Glu

405

410

415

gcc acc aag ccc acc cag cag agt ctg gtg ggt gtc ctg gag act gcc 1537

Ala Thr Lys Pro Thr Gln Gln Ser Leu Val Gly Val Leu Glu Thr Ala

420

425

430

atg aag ctg gcc aac cag gat gaa ggc cca gag gat gaa gag gat gag 1585

Met Lys Leu Ala Asn Gln Asp Glu Gly Pro Glu Asp Glu Glu Asp Glu

435

440

445

gtg cct aag aag cag aac agc cct gtg gcc ccc aca gcc cag ccc aaa 1633

Val Pro Lys Lys Gln Asn Ser Pro Val Ala Pro Thr Ala Gln Pro Lys

450

455

460

gcc cca ccc tca aga act ccc cag tcg gga tca gcc cca aca gcc aaa 1681

Ala Pro Pro Ser Arg Thr Pro Gln Ser Gly Ser Ala Pro Thr Ala Lys

465

470

475

480

gcg ccc ccc aaa gcc aca tcc acc aga gcc cag cag cag ctg gcc ttc 1729

Ala Pro Pro Lys Ala Thr Ser Thr Arg Ala Gln Gln Gln Leu Ala Phe

485

490

495

cta gag ggc cgc aag aag cag ctc ctg cag gcc gca ctg cga gcc aag 1777

Leu Glu Gly Arg Lys Lys Gln Leu Leu Gln Ala Ala Leu Arg Ala Lys

500

505

510

cag aaa aac gac gtg gag ggt gcc aag atg cac ctg cgc caa gcc aag 1825

Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys

515	520	525	
gga ctg gag cct atg ctg gag gcc tcg cgc aat ggg ctg cct gtg gac			1873
Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp			
530	535	540	
atc acc aag gtg ccg cct gcc cct gtc aac aag gac gac ttt gcc ctg			1921
Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu			
545	550	555	560
gtc cag cgg cct ggc ccg ggt ctg tct cag gag gcc gcc cgg cgc tat			1969
Val Gln Arg Pro Gly Pro Gly Leu Ser Gln Glu Ala Ala Arg Arg Tyr			
	565	570	575
ggt gaa ctc acc aag ctc ata cgg cag cag cac gag atg tgc ctg aac			2017
Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn			
	580	585	590
cac tca aac caa ttc acc cag ctg ggc aac atc act gaa acc acc aag			2065
His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys			
	595	600	605
ttt gaa aag ttg gcg gag gac tgt aag cgg agc atg gac att ctg aag			2113
Phe Glu Lys Leu Ala Glu Asp Cys Lys Arg Ser Met Asp Ile Leu Lys			
	610	615	620
caa gcc ttc gtc cgg ggt ctc ccc acg ccc acc gcc cgc ttt gag caa			2161
Gln Ala Phe Val Arg Gly Leu Pro Thr Pro Thr Ala Arg Phe Glu Gln			
625	630	635	640

agg acc ttc agc gtc atc aag atc ttc cct gac ctc agc agc aac gac 2209

Arg Thr Phe Ser Val Ile Lys Ile Phe Pro Asp Leu Ser Ser Asn Asp

645

650

655

atg ctc ctc ttc atc gtg aag ggc atc aac ttg ccc aca ccc cca gga 2257

Met Leu Leu Phe Ile Val Lys Gly Ile Asn Leu Pro Thr Pro Pro Gly

660

665

670

ctg tcc cct ggc gat ctg gat gtc ttt gtt cgg ttt gac ttc ccc tat 2305

Leu Ser Pro Gly Asp Leu Asp Val Phe Val Arg Phe Asp Phe Pro Tyr

675

680

685

ccc aac gtg gaa gaa gct cag aaa gac aag acc agt gtg atc aag aac 2353

Pro Asn Val Glu Glu Ala Gln Lys Asp Lys Thr Ser Val Ile Lys Asn

690

695

700

aca gac tcc cct gag ttc aag gag cag ttc aaa ctc tgc atc aac cgc 2401

Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg

705

710

715

720

agc cac cgt ggc ttc cga agg gcc atc cag acc aag ggc atc aag ttc 2449

Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe

725

730

735

gaa gtg gtt cac aag ggg ggg ctg ttc aag act gac cgg gtg ctg ggg 2497

Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly

740

745

750

aca gcc cag ctg aag ctg gat gca ctg gag ata gca tgt gag gtc cgg 2545
 Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg
 755 760 765

gag atc ctt gag gtc ctg gat ggt cgc cgg ccc aca ggg ggg cga ctg 2593
 Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu
 770 775 780

gag gta atg gtc cgg att cgg gag cca ctg aca gcc cag cag ttg gag 2641
 Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu
 785 790 795 800

acg acg aca gag agg tgg ctg gtc att gac cct gtg ccg gca gct gtg 2689
 Thr Thr Thr Glu Arg Trp Leu Val Ile Asp Pro Val Pro Ala Ala Val
 805 810 815

ccc aca cag gtt gct ggg ccc aaa ggg aag gcc cct cct gtg cct gcc 2737
 Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala
 820 825 830

cct gca agg gag tca ggg aac aga tca gcc cgg ccc ctg cat agc ctc 2785
 Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu
 835 840 845

agt gtg ctg gcg ttt gac caa gag cgt ctg gag cgg aag atc ctg gcc 2833
 Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala
 850 855 860

ctc agg cag gcg cgg cgg ccg gtg ccc cca gaa gtg gcc cag cag tac 2881
 689/754

Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr
865 870 875 880

cag gac atc atg caa cgc agc cag tgg cag agg gca cag ctg gag cag 2929
Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln
885 890 895

ggg ggt gtg ggc atc cga cgg gaa tac aca gcc cag ctg gag cgg cag 2977
Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln
900 905 910

ctg cag ttc tac acg gag gct gcc cgg cgc ctg ggc aac gat ggc agc 3025
Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser
915 920 925

agg gat gct gca aag gag gcg ctc tat agg cgg aat ctg gta ggg agt 3073
Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser
930 935 940

gag ctg cag cgg ctc cgc agg tgaggagccc atggggcggg cagccccag 3124
Glu Leu Gln Arg Leu Arg Arg
945 950

aaagcgggca gcaggccccg ataccgggaa gagccgacac agccacgaac cagacaagca 3184

gacaatcagc ggacaatcgg ttctggactc acccctcacc cgggccccca gccccgccag 3244

agcctccgtg gctgcgggtg ttgggaacca tgctgccag ccagtatgtg cccctcaccc 3304

aggcctggct gggccctgga gagtcctgtt tgcacagccc aggggtgtcc ggcctctggc 3364

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cttcctgttc ctccccagcc ttaaccccaa agccctcctg caccctaaag aagccactga 3484

ggctggccga gccacactgt ctccccaggg gcgtcgacct ggcccagctg ggtccccagg 3544

ccagcacatg gaataaaata gccagggcca cactc 3579

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<211> 951

<212> PRT

<213> Homo sapiens

<400> 172

Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala

1 5 10 15

Ala Ala Arg Gln Leu Gly Leu Leu Val Asp Leu Ser Pro Asp Gly Leu

20 25 30

Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe

35 40 45

Leu Ala Leu Val Gly Gly Gln Pro Pro Ala Leu Glu Lys Leu Lys Gly

50 55 60

Lys Gly Pro Leu Pro Met Glu Ala Ile Glu Lys Met Ala Ser Leu Cys
65 70 75 80

Met Arg Asp Pro Asp Glu Asp Glu Glu Glu Gly Thr Asp Glu Asp Asp
85 90 95

Leu Glu Ala Asp Asp Asp Leu Leu Ala Glu Leu Asn Glu Val Leu Gly
100 105 110

Glu Glu Gln Lys Ala Ser Glu Thr Pro Pro Pro Val Ala Gln Pro Lys
115 120 125

Pro Glu Ala Pro His Pro Gly Leu Glu Thr Thr Leu Gln Glu Arg Leu
130 135 140

Ala Leu Tyr Gln Thr Ala Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser
145 150 155 160

Ala Lys Met Arg Arg Tyr Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu
165 170 175

Leu Ala Ser Ile Arg Lys Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro
180 185 190

Pro Pro Val Ala Ile Gly Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser
195 200 205

Pro Ala Pro Thr Gln Pro Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro
210 215 220

Arg Val Thr Leu Glu Gly Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro
225 230 235 240

Gly Leu Ala Lys Pro Gln Met Pro Pro Gly Pro Cys Ser Pro Gly Pro
245 250 255

Leu Ala Gln Leu Gln Ser Arg Gln Arg Asp Tyr Lys Leu Ala Ala Leu
260 265 270

His Ala Lys Gln Gln Gly Asp Thr Thr Ala Ala Ala Arg His Phe Arg
275 280 285

Val Ala Lys Ser Phe Asp Ala Val Leu Glu Ala Leu Ser Arg Gly Glu
290 295 300

Pro Val Asp Leu Ser Cys Leu Pro Pro Pro Pro Asp Gln Leu Pro Pro
305 310 315 320

Asp Pro Pro Ser Pro Pro Ser Gln Pro Pro Thr Pro Ala Thr Ala Pro
325 330 335

Ser Thr Thr Glu Val Pro Pro Pro Pro Arg Thr Leu Leu Glu Ala Leu
340 345 350

Glu Gln Arg Met Glu Arg Tyr Gln Val Ala Ala Ala Gln Ala Lys Ser
355 360 365

Lys Gly Asp Gln Arg Lys Ala Arg Met His Glu Arg Ile Val Lys Gln
693/754

370	375	380	
Tyr Gln Asp Ala Ile Arg Ala His Lys Ala Gly Arg Ala Val Asp Val			
385	390	395	400
Ala Glu Leu Pro Val Pro Pro Gly Phe Pro Pro Ile Gln Gly Leu Glu			
	405	410	415
Ala Thr Lys Pro Thr Gln Gln Ser Leu Val Gly Val Leu Glu Thr Ala			
	420	425	430
Met Lys Leu Ala Asn Gln Asp Glu Gly Pro Glu Asp Glu Glu Asp Glu			
	435	440	445
Val Pro Lys Lys Gln Asn Ser Pro Val Ala Pro Thr Ala Gln Pro Lys			
	450	455	460
Ala Pro Pro Ser Arg Thr Pro Gln Ser Gly Ser Ala Pro Thr Ala Lys			
465	470	475	480
Ala Pro Pro Lys Ala Thr Ser Thr Arg Ala Gln Gln Gln Leu Ala Phe			
	485	490	495
Leu Glu Gly Arg Lys Lys Gln Leu Leu Gln Ala Ala Leu Arg Ala Lys			
	500	505	510
Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys			
	515	520	525

Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp
530 535 540

Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu
545 550 555 560

Val Gln Arg Pro Gly Pro Gly Leu Ser Gln Glu Ala Ala Arg Arg Tyr
565 570 575

Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn
580 585 590

His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys
595 600 605

Phe Glu Lys Leu Ala Glu Asp Cys Lys Arg Ser Met Asp Ile Leu Lys
610 615 620

Gln Ala Phe Val Arg Gly Leu Pro Thr Pro Thr Ala Arg Phe Glu Gln
625 630 635 640

Arg Thr Phe Ser Val Ile Lys Ile Phe Pro Asp Leu Ser Ser Asn Asp
645 650 655

Met Leu Leu Phe Ile Val Lys Gly Ile Asn Leu Pro Thr Pro Pro Gly
660 665 670

Leu Ser Pro Gly Asp Leu Asp Val Phe Val Arg Phe Asp Phe Pro Tyr
675 680 685

695/754

Pro Asn Val Glu Glu Ala Gln Lys Asp Lys Thr Ser Val Ile Lys Asn
690 695 700

Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg
705 710 715 720

Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe
725 730 735

Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly
740 745 750

Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg
755 760 765

Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu
770 775 780

Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu
785 790 795 800

Thr Thr Thr Glu Arg Trp Leu Val Ile Asp Pro Val Pro Ala Ala Val
805 810 815

Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala
820 825 830

Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu
696/754

835	840	845
Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala		
850	855	860
Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr		
865	870	875 880
Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln		
885	890	895
Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln		
900	905	910
Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser		
915	920	925
Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser		
930	935	940
Glu Leu Gln Arg Leu Arg Arg		
945	950	

<210> 173

<211> 2796

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (574)..(1683)

<400> 173

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tagtccttaa caaagggaag gcgataaatg taaataagct cacattttca gaatgagcgg 180
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cctgtttttt gttttttgtt ttgttttgtt ttgttttttt atggataaaa atatgcgctt 300
ccgaagtgcg agttgccagt ttacacgttt attagctaac tatctacagg catgagcaca 360
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ctccagaaaa ttcatgatt atccaagtct cagataaatc tgggtgccaga gtttggtttg 480
aactaactaa tgaagaaagc attctctact ggtcctcagt ctcaagagtg gtgaaccctt 540
gcacctagca ggctctctgg gaaaaaaaaa tcc atg ggt gac aga aga ttt att 594

Met Gly Asp Arg Arg Phe Ile

1

5

gac ttc caa ttc caa gat tta aat tca agt ctc aga ccc agg ttg gga 642
Asp Phe Gln Phe Gln Asp Leu Asn Ser Ser Leu Arg Pro Arg Leu Gly

10	15	20	
aat gca act gcc aat aat act tgc att gtt gat gat tcc ttc aag tat			690
Asn Ala Thr Ala Asn Asn Thr Cys Ile Val Asp Asp Ser Phe Lys Tyr			
25	30	35	
aat ttg aat ggt gct gtc tat agt gtt gta ttc atc ctg ggt cta ata			738
Asn Leu Asn Gly Ala Val Tyr Ser Val Val Phe Ile Leu Gly Leu Ile			
40	45	50	55
acc aac agt gcc tcc ctg ttt gtc ttc tgc ttc cgc atg aaa atg aga			786
Thr Asn Ser Ala Ser Leu Phe Val Phe Cys Phe Arg Met Lys Met Arg			
	60	65	70
agt gag acg gct act ttc atc acc aac ctg gcc ctc tct gat ttg ctt			834
Ser Glu Thr Ala Thr Phe Ile Thr Asn Leu Ala Leu Ser Asp Leu Leu			
	75	80	85
ttt gtt tgt acc cta cct ttc aaa ata ttt tac aac ttt aat cgc cac			882
Phe Val Cys Thr Leu Pro Phe Lys Ile Phe Tyr Asn Phe Asn Arg His			
	90	95	100
tgg cct ttt ggt gac acc ctc tgt aag atc tca ggg act gcg ttc ctc			930
Trp Pro Phe Gly Asp Thr Leu Cys Lys Ile Ser Gly Thr Ala Phe Leu			
105	110	115	
acc aac atc tat ggg agc atg ctc ttc ctc acc tgc atc agt gtg gat			978
Thr Asn Ile Tyr Gly Ser Met Leu Phe Leu Thr Cys Ile Ser Val Asp			
120	125	130	135

cgt ttc cta gcc att gtc tat ccc ttc cga tcg cgt acc atc agg acc 1026
 Arg Phe Leu Ala Ile Val Tyr Pro Phe Arg Ser Arg Thr Ile Arg Thr

140 145 150

agg agg aat tcc gcc att gtg tgc gct gga gtc tgg atc cta gtc ctc 1074
 Arg Arg Asn Ser Ala Ile Val Cys Ala Gly Val Trp Ile Leu Val Leu

155 160 165

agt ggt ggt att tca gct tct ttg ttc tcc acc act aat gtc aac aat 1122
 Ser Gly Gly Ile Ser Ala Ser Leu Phe Ser Thr Thr Asn Val Asn Asn

170 175 180

gcg acc acc act tgc ttt gaa ggc ttc tcc aaa cgt gtc tgg aag aca 1170
 Ala Thr Thr Thr Cys Phe Glu Gly Phe Ser Lys Arg Val Trp Lys Thr

185 190 195

tac ctg tcc aag atc act ata ttc att gaa gtt gtt gga ttc atc att 1218
 Tyr Leu Ser Lys Ile Thr Ile Phe Ile Glu Val Val Gly Phe Ile Ile

200 205 210 215

cct ctg ata ttg aat gtt tct tgt tct tct gtg gtg ctt aga acc ctc 1266
 Pro Leu Ile Leu Asn Val Ser Cys Ser Ser Val Val Leu Arg Thr Leu

220 225 230

cgc aag cct gca aca ttg tct cag att ggg acc aat aag aaa aaa gtg 1314
 Arg Lys Pro Ala Thr Leu Ser Gln Ile Gly Thr Asn Lys Lys Lys Val

235 240 245

ttg aag atg atc aca gtg cat atg gca gtg ttt gtg gta tgc ttt gta 1362
 Leu Lys Met Ile Thr Val His Met Ala Val Phe Val Val Cys Phe Val

250 255 260

cca tac aac tcc gtt ctc ttt tta tat gcc ttg gta cgc tcc caa gcc 1410
 Pro Tyr Asn Ser Val Leu Phe Leu Tyr Ala Leu Val Arg Ser Gln Ala

265 270 275

att act aat tgc tta ttg gaa agg ttt gca aag atc atg tac cca att 1458
 Ile Thr Asn Cys Leu Leu Glu Arg Phe Ala Lys Ile Met Tyr Pro Ile

280 285 290 295

acc ttg tgc ctt gca act ctg aat tgt tgc ttt gat cct ttt atc tat 1506
 Thr Leu Cys Leu Ala Thr Leu Asn Cys Cys Phe Asp Pro Phe Ile Tyr

300 305 310

tac ttc act ctt gaa tcc ttt cag aag tcc ttt tat atc aat aca cat 1554
 Tyr Phe Thr Leu Glu Ser Phe Gln Lys Ser Phe Tyr Ile Asn Thr His

315 320 325

ata agg atg gag tcg ctg ttt aag act gag aca cct ctg acc ccc aaa 1602
 Ile Arg Met Glu Ser Leu Phe Lys Thr Glu Thr Pro Leu Thr Pro Lys

330 335 340

cct tcc ctt cca gct atc caa gag gaa gtt agt gat caa aca aca aat 1650
 Pro Ser Leu Pro Ala Ile Gln Glu Glu Val Ser Asp Gln Thr Thr Asn

345 350 355

aat ggt ggt gaa tta atg ctg gaa tcc acc ttc taggtaccag aattgtcttt 1703

Asn Gly Gly Glu Leu Met Leu Glu Ser Thr Phe

360

365

370

caggttcagc tacagtgtct cttatgattt ttttcctatg ctataaatag gagaaacaaa 1763

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gaacactatt gtacatatc tgttttgttc agtaattata ggtcaagtct aattacaaca 1883

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aagatgtgta cat 2796

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<211> 370

<212> PRT

<213> Mus musculus

<400> 174

Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Leu Asn Ser

1 5 10 15

Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile

20 25 30

Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val

35 40 45

Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Ala Ser Leu Phe Val Phe

50	55	60
Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Thr Phe Ile Thr Asn		
65	70	75 80
Leu Ala Leu Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile		
	85	90 95
Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys		
100	105	110
Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe		
115	120	125
Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe		
130	135	140
Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala		
145	150	155 160
Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe		
	165	170 175
Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe		
180	185	190
Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile		
195	200	205

Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser
210 215 220

Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile
225 230 235 240

Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala
245 250 255

Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr
260 265 270

Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Leu Leu Glu Arg Phe
275 280 285

Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys
290 295 300

Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys
305 310 315 320

Ser Phe Tyr Ile Asn Thr His Ile Arg Met Glu Ser Leu Phe Lys Thr
325 330 335

Glu Thr Pro Leu Thr Pro Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu
340 345 350

Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser
355 360 365

Thr Phe

370

<210> 175

<211> 2299

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67).. (1176)

<400> 175

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Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser

1

5

10

aat tca agc ctc aga ccc agg ttg ggc aat gct act gcc aat aat act 156

Asn Ser Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr

15

20

25

30

tgc att gtt gat gat tcc ttc aag tat aat ctc aat ggt gct gtc tac 204

Cys Ile Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr

35

40

45

agt gtt gta ttc atc ttg ggt ctg ata acc aac agt gtc tct ctg ttt 252
 Ser Val Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe
 50 55 60

gtc ttc tgt ttc cgc atg aaa atg aga agt gag act gct att ttt atc 300
 Val Phe Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile
 65 70 75

acc aat cta gct gtc tct gat ttg ctt ttt gtc tgt aca cta cct ttt 348
 Thr Asn Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe
 80 85 90

aaa ata ttt tac aac ttc aac cgc cac tgg cct ttt ggt gac acc ctc 396
 Lys Ile Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu
 95 100 105 110

tgc aag atc tct gga act gca ttc ctt acc aac atc tat ggg agc atg 444
 Cys Lys Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met
 115 120 125

ctc ttt ctc acc tgt att agt gtg gat cgt ttc ctg gcc att gtc tat 492
 Leu Phe Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr
 130 135 140

cct ttt cga tct cgt act att agg act agg agg aat tct gcc att gtg 540
 Pro Phe Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val
 145 150 155

tgt gct ggt gtc tgg atc cta gtc ctc agt ggc ggt att tca gcc tct 588

Cys Ala Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser
160 165 170

ttg ttt tcc acc act aat gtc aac aat gca acc acc acc tgc ttt gaa 636
Leu Phe Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu
175 180 185 190

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Gly Phe Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile
195 200 205

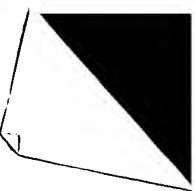
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Phe Ile Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser
210 215 220

tgc tct tct gtg gtg ctg aga act ctt cgc aag cct gct act ctg tct 780
Cys Ser Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser
225 230 235

caa att ggg acc aat aag aaa aaa gta ctg aaa atg atc aca gta cat 828
Gln Ile Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His
240 245 250

atg gca gtc ttt gtg gta tgc ttt gta ccc tac aac tct gtc ctc ttc 876
Met Ala Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe
255 260 265 270

ttg tat gcc ctg gtg cgc tcc caa gct att act aat tgc ttt ttg gaa 924
Leu Tyr Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu



275 280 285

aga ttt gca aag atc atg tac cca atc acc ttg tgc ctt gca act ctg 972
Arg Phe Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu
290 295 300

aac tgt tgt ttt gac cct ttc atc tat tac ttc acc ctt gaa tcc ttt 1020
Asn Cys Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe
305 310 315

cag aag tcc ttc tac atc aat gcc cac atc aga atg gag tcc ctg ttt 1068
Gln Lys Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe
320 325 330

aag act gaa aca cct ttg acc aca aag cct tcc ctt cca gct att caa 1116
Lys Thr Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln
335 340 345 350

gag gaa gtg agt gat caa aca aca aat aat ggt ggt gaa tta atg cta 1164
Glu Glu Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu
355 360 365

gaa tcc acc ttt taggtatgag aaatgtgttc aggtccagat atggtttctc 1216
Glu Ser Thr Phe
370

ctataat ttt tcctatgcta taaactaaag atttgaagct aatgatactg agaataatgc 1276

accaaatecca gtcagataca tttgtttgaa ggtatactgt agagttttta ttgctgtttt 1336

gttcagtaat tatagggtcaa atctaattac aacaaccaag atggattgcc aaactcttct 1396

gcttggttgg aatttcattg tatcgatta tccagggtgc tagtggcatt tgataatata 1456

gagatgactt tgaaactttc aaaaaggat ttctattcca atgatatttg gtaattaggt 1516

tgggcctata aatatagaac aaattcaggg atttttaaaa aattgtgtta ctactgatat 1576

atgctagttt tattttattt ttttgactg tcattgagtt tatttttagca caagaatatt 1636

tttagcctaa cattattaat aagaaatgtg tcaaattttt aacattggta aaatatgtta 1696

tgtgcatttt gaaaacagaa aacaaattgc gttggcatgt acgtgggtgg gaagaaaaag 1756

aaaattaaca ggatttacac aattataatc accagcagtg tgagttaaaa aaacttcggt 1816

gtttttacac caaattaaaa ttttcatgtc aaacttcaaa gccagaaagc tgctaaatac 1876

gtgtctggca ggtaaaagct ggaaaattac ttaaaacagg aaagtgtcaa taaaaaaact 1936

tgagcaacac caacatattt tttcttaaaa tgtcacgtta tcttcatttt gggaaactag 1996

gttctataaa atatttatcc tccctgttat actttggagc acagcacagc cagaaagggg 2056

ctgcatttgt gcccagggtca ggagcaaatt gaaaaaaaaa ataaagtaat actaaaaaat 2116

caactataa acccaaaaaca tttattaaaa cctgaattaa tccttttttg agggaggagt 2176

agagatatat aacctgaaaa tacttattct ttcttatcga attttggagc ctaatatagc 2236

caggagctgc tgaatttgtg cccctggatt ggaaccaaatt aaaaaaaaaa aaaaaaaatt 2296

cct 2299

<210> 176

<211> 370

<212> PRT

<213> Homo sapiens

<400> 176

Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser Asn Ser

1 5 10 15

Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile

20 25 30

Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val

35 40 45

Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe Val Phe

50 55 60

Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile Thr Asn

65 70 75 80

Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile

	85	90	95
Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys			
	100	105	110
Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe			
	115	120	125
Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe			
	130	135	140
Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala			
145	150	155	160
Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe			
	165	170	175
Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe			
	180	185	190
Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile			
	195	200	205
Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser			
	210	215	220
Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile			
225	230	235	240

Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala
245 250 255

Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr
260 265 270

Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu Arg Phe
275 280 285

Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys
290 295 300

Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys
305 310 315 320

Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe Lys Thr
325 330 335

Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu
340 345 350

Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser
355 360 365

Thr Phe
370

<210> 177

<211> 973

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (30)..(416)

<400> 177

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Met Ala Arg Gly Ser Leu Arg Arg

1

5

ttg ctg cgg ctc ctc gtg ctg ggg ctc tgg ctg gcg ttg ctg cgc tcc 101

Leu Leu Arg Leu Leu Val Leu Gly Leu Trp Leu Ala Leu Leu Arg Ser

10

15

20

gtg gcc ggg gag caa gcg cca ggc acc gcc ccc tgc tcc cgc ggc agc 149

Val Ala Gly Glu Gln Ala Pro Gly Thr Ala Pro Cys Ser Arg Gly Ser

25

30

35

40

tcc tgg agc gcg gac ctg gac aag tgc atg gac tgc gcg tct tgc agg 197

Ser Trp Ser Ala Asp Leu Asp Lys Cys Met Asp Cys Ala Ser Cys Arg

45

50

55

gcg cga ccg cac agc gac ttc tgc ctg ggc tgc gct gca gca cct cct 245

Ala Arg Pro His Ser Asp Phe Cys Leu Gly Cys Ala Ala Ala Pro Pro

60

65

70

gcc ccc ttc cgg ctg ctt tgg ccc atc ctt ggg ggc gct ctg agc ctg 293
 Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu Gly Gly Ala Leu Ser Leu

75

80

85

acc ttc gtg ctg ggg ctg ctt tct ggc ttt ttg gtc tgg aga cga tgc 341
 Thr Phe Val Leu Gly Leu Leu Ser Gly Phe Leu Val Trp Arg Arg Cys

90

95

100

cgc agg aga gag aag ttc acc acc ccc ata gag gag acc ggc gga gag 389
 Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile Glu Glu Thr Gly Gly Glu

105

110

115

120

ggc tgc cca gct gtg gcg ctg atc cag tgacaatgtg cccctgcca 436
 Gly Cys Pro Ala Val Ala Leu Ile Gln

125

gccggggctc gcccaactcat cattcattca tccattctag agccagtctc tgcctcccag 496

acgcggcggg agccaagctc ctccaaccac aaggggggtg gggggcgggtg aatcacctcc 556

gaggcctggg tccagggttc aggggaacct tccaaggtgt ctggttgccc tgcctctggc 616

tccagaacag aaaggagacc tcacgctggc tcacacaaaa cagctgacac tgactaagga 676

actgcagcat ttgcacaggg gaggggggtg ccctccttcc tagaggccct gggggccagg 736

ctgacttggg gggcagactt gacactaggc cccactcact cagatgtcct gaaattccac 796

cacgggggtc accctggggg gttagggacc tatttttaac actagggggc tggcccacta 856

ggagggctgg ccctaagata cagaccccc caactcccca aagcggggag gagatattta 916

ttttggggag agtttgagg ggagggagaa tttattaata aaagaatctt taacttt 973

<210> 178

<211> 129

<212> PRT

<213> Homo sapiens

<400> 178

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Leu	Trp	Leu	Ala	Leu	Leu	Arg	Ser	Val	Ala	Gly	Glu	Gln	Ala	Pro	Gly
				20					25					30	

Thr	Ala	Pro	Cys	Ser	Arg	Gly	Ser	Ser	Trp	Ser	Ala	Asp	Leu	Asp	Lys
			35					40					45		

Cys	Met	Asp	Cys	Ala	Ser	Cys	Arg	Ala	Arg	Pro	His	Ser	Asp	Phe	Cys
		50					55						60		

Leu	Gly	Cys	Ala	Ala	Ala	Pro	Pro	Ala	Pro	Phe	Arg	Leu	Leu	Trp	Pro
	65					70					75				80

Ile	Leu	Gly	Gly	Ala	Leu	Ser	Leu	Thr	Phe	Val	Leu	Gly	Leu	Leu	Ser
					85						90				95

Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
100 105 110

Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile
115 120 125

Gln

<210> 179

<211> 3631

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (191)..(3244)

<400> 179

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ccacctggaa gggaaccgcc ttgtttctcac ctgccttgcc gaaggagct ggcctttgga 180

gttcaagtgg atg cgc gat gac agt gag ctc acc acc tac agc agc gaa 229

Met Arg Asp Asp Ser Glu Leu Thr Thr Tyr Ser Ser Glu

1	5	10	
tat aag tac att att cca tct ttg cag aag ctc gat gct ggg ttt tac	277		
Tyr Lys Tyr Ile Ile Pro Ser Leu Gln Lys Leu Asp Ala Gly Phe Tyr			
15	20	25	
cgc tgc gtg gtg cga aac aga atg gga gca ctc ctg caa aga aaa tca	325		
Arg Cys Val Val Arg Asn Arg Met Gly Ala Leu Leu Gln Arg Lys Ser			
30	35	40	45
gaa gtt caa gtc gca tat atg gga agt ttc atg gat acg gac cag agg	373		
Glu Val Gln Val Ala Tyr Met Gly Ser Phe Met Asp Thr Asp Gln Arg			
50	55	60	
aaa aca gtt tct caa gga cgt gca gcg att cta aac ctg ctg ccc atc	421		
Lys Thr Val Ser Gln Gly Arg Ala Ala Ile Leu Asn Leu Leu Pro Ile			
65	70	75	
acc agc tac ccc aga cct caa gtg act tgg ttt aga gaa ggg cac aag	469		
Thr Ser Tyr Pro Arg Pro Gln Val Thr Trp Phe Arg Glu Gly His Lys			
80	85	90	
att att cca agc aac aga ata gcc atc aca ttg gag aat cag ctg gtg	517		
Ile Ile Pro Ser Asn Arg Ile Ala Ile Thr Leu Glu Asn Gln Leu Val			
95	100	105	
atc ctc gcc acc aca acc agt gat gcc ggg gca tac tac gtg cag gcc	565		
Ile Leu Ala Thr Thr Thr Ser Asp Ala Gly Ala Tyr Tyr Val Gln Ala			
110	115	120	125

gtg aat gag aaa aat gga gaa aac aag aca agc cca ttc att cat ttg	613
Val Asn Glu Lys Asn Gly Glu Asn Lys Thr Ser Pro Phe Ile His Leu	
130 135 140	
agc ata gca aga gat gtt ggc aca cct gaa acc atg gcc cca acc att	661
Ser Ile Ala Arg Asp Val Gly Thr Pro Glu Thr Met Ala Pro Thr Ile	
145 150 155	
gtg gtt ccc ccg ggc aac aga agt gtg gtg gct gga tcc agt gag acc	709
Val Val Pro Pro Gly Asn Arg Ser Val Val Ala Gly Ser Ser Glu Thr	
160 165 170	
acc ttg gaa tgt ata gcc agt gcc agg cct gtg gag gac ctg agt gtg	757
Thr Leu Glu Cys Ile Ala Ser Ala Arg Pro Val Glu Asp Leu Ser Val	
175 180 185	
acc tgg aag agg aat gga gtg aga atc acc agt ggc ctc cac agc ttt	805
Thr Trp Lys Arg Asn Gly Val Arg Ile Thr Ser Gly Leu His Ser Phe	
190 195 200 205	
gga aga cgc ctc acc atc agc aac ccg acg tcc gcg gac acc ggg cca	853
Gly Arg Arg Leu Thr Ile Ser Asn Pro Thr Ser Ala Asp Thr Gly Pro	
210 215 220	
tac gtc tgc gag gcg gcg ctg ccg ggg agc gct ttt gaa ccg gcc agg	901
Tyr Val Cys Glu Ala Ala Leu Pro Gly Ser Ala Phe Glu Pro Ala Arg	
225 230 235	

gcg acg gcc ttt ctt ttc atc ata gag cca cca tat ttt act gct gag	949
Ala Thr Ala Phe Leu Phe Ile Ile Glu Pro Pro Tyr Phe Thr Ala Glu	
240 245 250	
ccc gag agt cgg att tca gct gaa gta gaa gaa act gtg gac atc gga	997
Pro Glu Ser Arg Ile Ser Ala Glu Val Glu Glu Thr Val Asp Ile Gly	
255 260 265	
tgt caa gcc atg ggg gtc ccc ctt ccc acc ctc cag tgg tac aag gat	1045
Cys Gln Ala Met Gly Val Pro Leu Pro Thr Leu Gln Trp Tyr Lys Asp	
270 275 280 285	
gcc atc tcc atc agc agg ctc cag aat cct cga tac aaa gtg ctc gcc	1093
Ala Ile Ser Ile Ser Arg Leu Gln Asn Pro Arg Tyr Lys Val Leu Ala	
290 295 300	
agc gga ggc ctg cgc atc cag aag ctg cgt cca gag gac tcc gga atc	1141
Ser Gly Gly Leu Arg Ile Gln Lys Leu Arg Pro Glu Asp Ser Gly Ile	
305 310 315	
ttc cag tgc ttc gcc agc aat gaa gga ggg gag atc cag acc cac acc	1189
Phe Gln Cys Phe Ala Ser Asn Glu Gly Gly Glu Ile Gln Thr His Thr	
320 325 330	
tac ctg gat gta acc aat atc gct cca gtg ttc acc cag cgg cca gtg	1237
Tyr Leu Asp Val Thr Asn Ile Ala Pro Val Phe Thr Gln Arg Pro Val	
335 340 345	
gac acc aca gtt act gac ggg atg aca gcc att cta agg tgt gag gtg	1285

Asp Thr Thr Val Thr Asp Gly Met Thr Ala Ile Leu Arg Cys Glu Val
 350 355 360 365

tcc ggg gct ccc aaa ccc gcc atc acc tgg aaa aga gaa aac cac att 1333
 Ser Gly Ala Pro Lys Pro Ala Ile Thr Trp Lys Arg Glu Asn His Ile
 370 375 380

ctg gcc agt ggc tct gtc cgg att cct agg ttc atg ctt ctt gaa tcg 1381
 Leu Ala Ser Gly Ser Val Arg Ile Pro Arg Phe Met Leu Leu Glu Ser
 385 390 395

ggg ggt cta cag atc gcg ccc gtc ttc atc cag gat gcc ggc aac tac 1429
 Gly Gly Leu Gln Ile Ala Pro Val Phe Ile Gln Asp Ala Gly Asn Tyr
 400 405 410

acc tgc tat gcg gcc aac aca gag ggc tcc ctg aat gca tcg gcc acg 1477
 Thr Cys Tyr Ala Ala Asn Thr Glu Gly Ser Leu Asn Ala Ser Ala Thr
 415 420 425

ctc act gtg tgg aat cgg acg tcc atc gtc cac cct cct gag gac cac 1525
 Leu Thr Val Trp Asn Arg Thr Ser Ile Val His Pro Pro Glu Asp His
 430 435 440 445

gtg gtg att aag ggg acc acg gcc acg ctg cac tgt ggt gcc aca cat 1573
 Val Val Ile Lys Gly Thr Thr Ala Thr Leu His Cys Gly Ala Thr His
 450 455 460

gac ccc cgg gtt tca ctc cgc tac gtt tgg aag aag gac aac gtg gcc 1621
 Asp Pro Arg Val Ser Leu Arg Tyr Val Trp Lys Lys Asp Asn Val Ala

465	470	475	
ctg act cca tcg agc acg tct agg atc gtg gtg gag aag gac ggg tcc			1669
Leu Thr Pro Ser Ser Thr Ser Arg Ile Val Val Glu Lys Asp Gly Ser			
480	485	490	
ctt ctc atc agc cag acg tgg tca ggc gac atc ggt gac tac agc tgc			1717
Leu Leu Ile Ser Gln Thr Trp Ser Gly Asp Ile Gly Asp Tyr Ser Cys			
495	500	505	
gag att gtt tct gaa gga ggg aat gac tcc agg atg gcc cgg ctg gaa			1765
Glu Ile Val Ser Glu Gly Gly Asn Asp Ser Arg Met Ala Arg Leu Glu			
510	515	520	525
gtg att gaa ctg cct cat tca cct cag aac ctc ctg gtc agc cct aat			1813
Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn			
530	535	540	
tct tcc cac agc cac gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat			1861
Ser Ser His Ser His Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp			
545	550	555	
gga aac agt cct att ctt tat tac atc gtg gag ctg tct gaa aac aac			1909
Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn			
560	565	570	
tct cca tgg aag gtg cat ctg tca aac gtt ggc cct gag atg aca ggc			1957
Ser Pro Trp Lys Val His Leu Ser Asn Val Gly Pro Glu Met Thr Gly			
575	580	585	

gtc acc gtg agt ggc ctg act ccg gct cgt acc tat caa ttc cgg gtg 2005

tgc gcg gtg aat gaa gtg ggc agg ggc cag tac agt gcc gag aca agc 2053

610 615 620

agg ttg atg cta cct gaa gaa cca ccc agt gct ccc ccg aaa aat ata 2101

625 630 635

gtg gcc agt ggg cgg act aat cag tcc att atg gtc cag tgg cag cca 2149

640 645 650

ccc cca gaa aca gag cac aac ggg gtg ttg cgt gga tac atc ctc agg 2197

655 660 665

tac cgc ctg gct ggc ctt ccc gga gag tac cag cag cgg aac atc acc 2245

670 675 680 685

agc ccg gag gtg aac tac tgc ctg gtg aca gac ctg atc atc tgg aca 2293

690 695 700

cag tat gag ata cag gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc 2341
 Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val

705

710

715

ttc agc agg gca gtg acc gag tac acc ttg cag gga gtg ccc acc gcg 2389
 Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala

720

725

730

ccc ccg cag aac gtg cag acg gaa gcc gtg aac tcc acc acc att cag 2437
 Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln

735

740

745

ttc ctg tgg aac cct ccg cct cag cag ttt atc aat ggc atc aac cag 2485
 Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln

750

755

760

765

gga tac aag ctt ctg gca tgg ccg gca gat gcc ccc gag gct gtc act 2533
 Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr

770

775

780

gtg gtc act att gcc cca gat ttc cac gga gtc cac cat gga cac ata 2581
 Val Val Thr Ile Ala Pro Asp Phe His Gly Val His His Gly His Ile

785

790

795

acg aac ctg aag aag ttt acc gcc tac ttc act tcc gtt ctg tgc ttc 2629
 Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe

800

805

810

acc acc cct ggg gac ggg cct ccc agc aca cct cag ctg gtc tgg act 2677

Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr	
815	820 825
cag gaa gac aaa cca gga gct gtg gga cat ctg agt ttc aca gag atc	2725
Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile	
830	835 840 845
ttg gac aca tct ctc aag gtc agc tgg cag gag ccc ctg gag aaa aat	2773
Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn	
850	855 860
ggc atc att act ggc tat cag atc tct tgg gaa gtg tac ggc agg aac	2821
Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn	
865	870 875
gac tct cgt ctc acg cac acc ctg aac agc acg acg cac gag tac aag	2869
Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys	
880	885 890
atc caa ggc ctc tca tct ctc acc acc tac acc atc gac gtg gcc gct	2917
Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala	
895	900 905
gtg act gcc gtg ggc act ggc ctg gtg act tca tcc acc att tct tct	2965
Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser	
910	915 920 925
gga gtg ccc cca gac ctt cct ggt gcc cca tcc aac ctg gtc att tcc	3013
Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser	

930	935	940	
aac atc agc cct cgc tcc gcc acc ctt cag ttc cgg cca ggc tat gac			3061
Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp			
945	950	955	
ggg aaa acg tcc atc tcc agg tgg att gtt gag ggg cag atg aga cat			3109
Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu Gly Gln Met Arg His			
960	965	970	
caa ggt gtt gga tta cct gcc gag gtc aca cag cca agc cat gaa gcc			3157
Gln Gly Val Gly Leu Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala			
975	980	985	
gga ttg gag cct gca aac ctc gga agt ctg tgg ctg ctc agc ctg gtg			3205
Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val			
990	995	1000	1005
tat tgg tgt tac agc cag aaa ctt tgg gaa ttc tct tgt tagttggtta			3254
Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe Ser Cys			
1010	1015		
gttttactgt aattttctat aaagaattca tatcatctgt taatggcgac agtttttgtt			3314
tcttcctttg aattttttat attcttttctt tctctttttt gtttcttctt ctttgagtat			3374
tttgtaatct tactgggagg gctaaagcgt cttctatcat atcgaattgg gacaatgata			3434
gaagacaatc tttgttttgt cactctaaag aaattattgt aagattttat catcaggtat			3494

gacatttaca ccattgatgt aggcttttta aaaaatatat ccagcctgta ttgggttaag 3554

atgattcttt tctgacctg atttcctagg agttggtttt ttttttttta aagcataaat 3614

aaattttaatt gcatcag 3631

<210> 180

<211> 1018

<212> PRT

<213> Homo sapiens

<400> 180

Met Arg Asp Asp Ser Glu Leu Thr Thr Tyr Ser Ser Glu Tyr Lys Tyr

1 5 10 15

Ile Ile Pro Ser Leu Gln Lys Leu Asp Ala Gly Phe Tyr Arg Cys Val

20 25 30

Val Arg Asn Arg Met Gly Ala Leu Leu Gln Arg Lys Ser Glu Val Gln

35 40 45

Val Ala Tyr Met Gly Ser Phe Met Asp Thr Asp Gln Arg Lys Thr Val

50 55 60

Ser Gln Gly Arg Ala Ala Ile Leu Asn Leu Leu Pro Ile Thr Ser Tyr

65 70 75 80

Pro Arg Pro Gln Val Thr Trp Phe Arg Glu Gly His Lys Ile Ile Pro
85 90 95

Ser Asn Arg Ile Ala Ile Thr Leu Glu Asn Gln Leu Val Ile Leu Ala
100 105 110

Thr Thr Thr Ser Asp Ala Gly Ala Tyr Tyr Val Gln Ala Val Asn Glu
115 120 125

Lys Asn Gly Glu Asn Lys Thr Ser Pro Phe Ile His Leu Ser Ile Ala
130 135 140

Arg Asp Val Gly Thr Pro Glu Thr Met Ala Pro Thr Ile Val Val Pro
145 150 155 160

Pro Gly Asn Arg Ser Val Val Ala Gly Ser Ser Glu Thr Thr Leu Glu
165 170 175

Cys Ile Ala Ser Ala Arg Pro Val Glu Asp Leu Ser Val Thr Trp Lys
180 185 190

Arg Asn Gly Val Arg Ile Thr Ser Gly Leu His Ser Phe Gly Arg Arg
195 200 205

Leu Thr Ile Ser Asn Pro Thr Ser Ala Asp Thr Gly Pro Tyr Val Cys
210 215 220

Glu Ala Ala Leu Pro Gly Ser Ala Phe Glu Pro Ala Arg Ala Thr Ala
225 230 235 240

Phe Leu Phe Ile Ile Glu Pro Pro Tyr Phe Thr Ala Glu Pro Glu Ser
245 250 255

Arg Ile Ser Ala Glu Val Glu Glu Thr Val Asp Ile Gly Cys Gln Ala
260 265 270

Met Gly Val Pro Leu Pro Thr Leu Gln Trp Tyr Lys Asp Ala Ile Ser
275 280 285

Ile Ser Arg Leu Gln Asn Pro Arg Tyr Lys Val Leu Ala Ser Gly Gly
290 295 300

Leu Arg Ile Gln Lys Leu Arg Pro Glu Asp Ser Gly Ile Phe Gln Cys
305 310 315 320

Phe Ala Ser Asn Glu Gly Gly Glu Ile Gln Thr His Thr Tyr Leu Asp
325 330 335

Val Thr Asn Ile Ala Pro Val Phe Thr Gln Arg Pro Val Asp Thr Thr
340 345 350

Val Thr Asp Gly Met Thr Ala Ile Leu Arg Cys Glu Val Ser Gly Ala
355 360 365

Pro Lys Pro Ala Ile Thr Trp Lys Arg Glu Asn His Ile Leu Ala Ser
370 375 380

Gly Ser Val Arg Ile Pro Arg Phe Met Leu Leu Glu Ser Gly Gly Leu

385	390	395	400
Gln Ile Ala Pro Val Phe Ile Gln Asp Ala Gly Asn Tyr Thr Cys Tyr			
	405	410	415
Ala Ala Asn Thr Glu Gly Ser Leu Asn Ala Ser Ala Thr Leu Thr Val			
	420	425	430
Trp Asn Arg Thr Ser Ile Val His Pro Pro Glu Asp His Val Val Ile			
	435	440	445
Lys Gly Thr Thr Ala Thr Leu His Cys Gly Ala Thr His Asp Pro Arg			
	450	455	460
Val Ser Leu Arg Tyr Val Trp Lys Lys Asp Asn Val Ala Leu Thr Pro			
465	470	475	480
Ser Ser Thr Ser Arg Ile Val Val Glu Lys Asp Gly Ser Leu Leu Ile			
	485	490	495
Ser Gln Thr Trp Ser Gly Asp Ile Gly Asp Tyr Ser Cys Glu Ile Val			
	500	505	510
Ser Glu Gly Gly Asn Asp Ser Arg Met Ala Arg Leu Glu Val Ile Glu			
	515	520	525
Leu Pro His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His			
	530	535	540

Ser His Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser
545 550 555 560

Pro Ile Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp
565 570 575

Lys Val His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val
580 585 590

Ser Gly Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val
595 600 605

Asn Glu Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met
610 615 620

Leu Pro Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser
625 630 635 640

Gly Arg Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu
645 650 655

Thr Glu His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu
660 665 670

Ala Gly Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu
675 680 685

Val Asn Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu
690 695 700

Ile Gln Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg
705 710 715 720

Ala Val Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln
725 730 735

Asn Val Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp
740 745 750

Asn Pro Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys
755 760 765

Leu Leu Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr
770 775 780

Ile Ala Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu
785 790 795 800

Lys Lys Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro
805 810 815

Gly Asp Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp
820 825 830

Lys Pro Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr
835 840 845

Ser Leu Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile
732/754

850	855	860
Thr Gly Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg		
865	870	875 880
Leu Thr His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys Ile Gln Gly		
	885	890 895
Leu Ser Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala		
	900	905 910
Val Gly Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro		
	915	920 925
Pro Asp Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser		
	930	935 940
Pro Arg Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr		
945	950	955 960
Ser Ile Ser Arg Trp Ile Val Glu Gly Gln Met Arg His Gln Gly Val		
	965	970 975
Gly Leu Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu		
	980	985 990
Pro Ala Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys		
	995	1000 1005

Tyr Ser Gln Lys Leu Trp Glu Phe Ser Cys

1010

1015

<210> 181

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 181

cttctgctct aaaagctgcg

20

<210> 182

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 182

cgacctgcag ctcgagcaca

20

<210> 183

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 183

ctagctagct agaaactact aaaatgtaaa tgacatag

38

<210> 184

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 184

cgcaagcttg aaaggttgca gttagaatgt cctttc

36

<210> 185

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<220>

<223> DNA/RNA molecule

<400> 185

guccaggaua ucaugaguct t

21

<210> 186

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<220>

<223> DNA/RNA molecule

<400> 186

gacucaugau auccuggact t

21

<210> 187

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<220>

<223> DNA/RNA molecule

<400> 187

gaagucugaa gaucuaucct t

21

<210> 188

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<220>

<223> DNA/RNA molecule

<400> 188

ggauagaucu ucagacuuct t

21

<210> 189

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<220>

<223> DNA/RNA molecule

<400> 189

gcugaagaag agguguucct t

21

<210> 190

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<220>

<223> DNA/RNA molecule

<400> 190

ggaacaccuc uucuucagct t

21

<210> 191

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<220>

<223> DNA/RNA molecule

<400> 191

gaugacacag augaagccct t

21

<210> 192

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<220>

<223> DNA/RNA molecule

<400> 192

gggcuucauc ugugucauct t

21

<210> 193

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<220>

<223> DNA/RNA molecule

<400> 193

gcccucagag uccagaauct t

21

<210> 194

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic

double stranded nucleic acid

<220>

<223> DNA/RNA molecule

<400> 194

gauucuggac ucugagggt t

21

<210> 195

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<220>

<223> DNA/RNA molecule

<400> 195

gaugacuuug guaucaaact t

21

<210> 196

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<220>

<223> DNA/RNA molecule

<400> 196

guuugauacc aaagucauct t

21

<210> 197

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 197

aaaagtccag gatatcatga gtctttttta

30

<210> 198

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 198

agcttaaaaa agactcatga ttcctggac

30

<210> 199

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 199

aaaagaagtc tgaagatcta tcctttttta

30

<210> 200

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 200

agcttaaaaa aggatagatc ttcagacttc

30

<210> 201

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 201

aaaagctgaa gaagaggtgt tcctttttta

30

<210> 202

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 202

agcttaaaaa aggaacacct cttcttcagc

30

<210> 203

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 203

aaaagatgac acagatgaag ccctttttta

30

<210> 204

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 204

agcttaaaaa agggcttcat ctgtgtcatc

30

<210> 205

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 205

aaaagccctc agagtccaga atctttttta

30

<210> 206

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 206

agcttaaaaa agattctgga ctctgagggc

30

<210> 207

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 207

aaaagatgac ttggtatca aactttttta

30

<210> 208

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic DNA

<400> 208

agcttaaaaa agtttgatac caaagtcac

30

<210> 209

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 209

gcgaattcgg gcaggaagag ggcctatttc ccat

34

<210> 210

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 210

gcaagctttt tttgtcttct ttccacaaga tatataaagc caag

44

<210> 211

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 211

cgctcgagcc atggaattcg aacgctgacg tc

32

<210> 212

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 212

gcaagctttc tcatacagaa cttataagat tccc

34

<210> 213

<211> 21

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<400> 213

guccaggaua ucaugaguc

19

<210> 214

<211> 21

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<400> 214

gacucaugau auccuggac

19

<210> 215

<211> 21

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<400> 215

gaagucugaa gaucuaucc

19

<210> 216

<211> 21

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<400> 216

ggauagaucu ucagacuuc

19

<210> 217

<211> 21

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<400> 217

gcugaagaag agguguucc

19

<210> 218

<211> 21

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<400> 218

ggaacaccuc uucuucagc

19

<210> 219

<211> 21

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<400> 219

gaugacacag augaagccc

19

<210> 220

<211> 21

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<400> 220

gggcuucauc ugugucauc

19

<210> 221

<211> 21

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<400> 221

gcccucagag uccagaauc

19

<210> 222

<211> 21

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<400> 222

gauucuggac ucugagggc

19

<210> 223

<211> 21

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<400> 223

gaugacuuug guaucaaac

19

<210> 224

<211> 21

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic
double stranded nucleic acid

<400> 224

guuugauacc aaagucauc

19